(FILE 'HOME' ENTERED AT 21:08:12 ON 02 AUG 2006)

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 21:08:27 ON
     02 AUG 2006
L1   16489 SEA ABB=ON PLU=ON MCCREADY P?/AU OR RADNEDGE L?/AU OR
                 ANDERSON G?/AU OR OTT L?/AU OR SLEZAK T?/AU OR KUCZMARSKI
                 T?/AU OR MOTIN V?/AU
L2   172 SEA ABB=ON PLU=ON L1 AND PESTIS
L3   37 SEA ABB=ON PLU=ON L2 AND (PRIMER OR PROBE OR PCR)
L4   16 DUP REM L3 (21 DUPLICATES REMOVED)
                 D L4 BIB ABS 1-16
L5   256 SEA ABB=ON PLU=ON PESTIS (50W) (PROBE OR PRIMER OR PCR)
L6   150 SEA ABB=ON PLU=ON L5 AND DETECT?
L7   82 DUP REM L6 (68 DUPLICATES REMOVED)

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	257	mccready-p$.in. radnedge-l$.in. andersen-g$.in. ott-l$.in. slezak-t$.in. kuczmarski-t$.in. motin-v$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:13
L2	11	1 and pestis	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:13
L3	131	Pestis same (primer probe PCR)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:14
L4	57	3 same (detect$8 determin$8 identif$8)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:14

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DEFINITION  Yersinia pestis KIM plasmid pMT1, complete sequence.
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VERSION     AF053947.1  GI:2996286
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SOURCE      Yersinia pestis KIM
  ORGANISM  Yersinia pestis KIM
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Yersinia.
REFERENCE   1  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
  TITLE     Structural organization of virulence-associated plasmids of
            Yersinia pestis
  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
   PUBMED   9748454
REFERENCE   2  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Carrano,A.V., Brubaker,R. and Garcia,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
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ACCESSION   AF053947
VERSION     AF053947.1  GI:2996286
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SOURCE      Yersinia pestis KIM
  ORGANISM  Yersinia pestis KIM
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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REFERENCE   1  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
  TITLE     Structural organization of virulence-associated plasmids of
            Yersinia pestis
  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
   PUBMED   9748454
REFERENCE   2  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Carrano,A.V., Brubaker,R. and Garcia,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
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ACCESSION   AF053947
VERSION     AF053947.1  GI:2996286
KEYWORDS    .
SOURCE      Yersinia pestis KIM
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            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Yersinia.
REFERENCE   1  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
  TITLE     Structural organization of virulence-associated plasmids of
            Yersinia pestis
  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
   PUBMED   9748454
REFERENCE   2  (bases 1 to 100984)
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  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
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Best Local Similarity    100.0%;   Pred. No. 5.6e-05;
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ACCESSION   AF053947
VERSION     AF053947.1  GI:2996286
KEYWORDS    .
SOURCE      Yersinia pestis KIM
  ORGANISM  Yersinia pestis KIM
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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REFERENCE   1  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
  TITLE     Structural organization of virulence-associated plasmids of
            Yersinia pestis
  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
   PUBMED   9748454
REFERENCE   2  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Carrano,A.V., Brubaker,R. and Garcia,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
            Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore,
            CA 94550, USA
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  TITLE     Structural organization of virulence-associated plasmids of
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  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
   PUBMED   9748454
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  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
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ACCESSION   AF053947
VERSION     AF053947.1  GI:2996286
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SOURCE      Yersinia pestis KIM
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            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Yersinia.
REFERENCE   1  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
  TITLE     Structural organization of virulence-associated plasmids of
            Yersinia pestis
  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
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  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Carrano,A.V., Brubaker,R. and Garcia,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
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LOCUS       AF053947                100984 bp    DNA     circular BCT 17-JUN-2003
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ACCESSION   AF053947
VERSION     AF053947.1  GI:2996286
KEYWORDS    .
SOURCE      Yersinia pestis KIM
  ORGANISM  Yersinia pestis KIM
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REFERENCE   1  (bases 1 to 100984)
  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
  TITLE     Structural organization of virulence-associated plasmids of
            Yersinia pestis
  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
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  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
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VERSION     AF053947.1  GI:2996286
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  AUTHORS   Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
  TITLE     Structural organization of virulence-associated plasmids of
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  JOURNAL   J. Bacteriol. 180 (19), 5192-5202 (1998)
   PUBMED   9748454
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  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology and Biotechnology Research,
            Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore,
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From:	Bausch, Sarae
Sent:	Thursday, June 29, 2006 2:57 PM
To:	STIC-Biotech/ChemLib
Subject:	10/630536 nucleic acid search

Please do a standard nucleic acid sequence for the following: SEQ ID No. 1-8 of 10/630536.
Please print out the first 100 hits.

Thank you.

Sarae Bausch, Ph.D.
USPTO Art Unit 1634
REM 2 A 70
Mailbox: REM 2 C 70
(571) 272-2912

Tracking:

Recipient	Read
STIC-Biotech/ChemLib	Read: 6/29/06 2:57 PM

1

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-1.rst.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-1.rst.

start

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                         GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:17:07 ; Search time 1015.7 Seconds
                                           (without alignments)
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Title:           US-10-630-536-1
Perfect score:   28
Sequence:        1 atttcccaccaatcaacgatacaagaat 28

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       EST:*
                 1:   gb_est1:*
                 2:   gb_est3:*
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                 14:  gb_gss4:*

         Pred. No. is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	20.6	73.6	375	14	AG254363	AG254363 Lotus cor
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c	5	20.6	73.6	875	12	CC657710	CC657710 OGDAG43TM
c	6	20.2	72.1	648	3	BU477783	BU477783 603844771
c	7	20	71.4	272	12	CG815211	CG815211 SOYEC63TV
	8	20	71.4	417	1	AA176882	AA176882 zp10e05.r
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	25	19.6	70.0	861	13	DU222493	DU222493 109857403
c	26	19.6	70.0	869	14	DU958392	DU958392 225547 To
	27	19.6	70.0	971	10	DV501436	DV501436 He_wd2a1_
	28	19.6	70.0	1005	12	BZ793314	BZ793314 PUGCC57TD
	29	19.6	70.0	1170	9	DR137600	DR137600 49220587
c	30	19.6	70.0	1217	12	CC301458	CC301458 CH261-69F
c	31	19.6	70.0	1501	12	CC263959	CC263959 CH261-184
	32	19.4	69.3	387	11	AQ030506	AQ030506 HS_2185_A
	33	19.4	69.3	398	4	CA814251	CA814251 CA48LN08I
	34	19.4	69.3	410	4	CA814674	CA814674 CA48LN10I
	35	19.4	69.3	430	5	CD801481	CD801481 EST 9390
	36	19.4	69.3	436	5	CF405344	CF405344 CSECS044C
c	37	19.4	69.3	472	5	CF608016	CF608016 GEMMA01_0
c	38	19.4	69.3	508	5	CF606064	CF606064 RADIC01_0
c	39	19.4	69.3	518	4	CB911407	CB911407 VVD130G06
	40	19.4	69.3	534	8	CN546235	CN546235 EST 18187
	41	19.4	69.3	553	10	DV941324	DV941324 CSECS214A
	42	19.4	69.3	556	4	CA813934	CA813934 CA48LN07I
	43	19.4	69.3	612	4	CA814125	CA814125 CA48LN08I
c	44	19.4	69.3	617	4	CA816560	CA816560 CA12EI304
c	45	19.4	69.3	622	4	CA813069	CA813069 CA48LN08I
	46	19.4	69.3	664	5	CK906580	CK906580 CSECS160D
	47	19.4	69.3	681	4	CB340835	CB340835 CA23EI01I
	48	19.4	69.3	686	4	CA809249	CA809249 CA12LIO2I
c	49	19.4	69.3	693	8	CV100606	CV100606 FAMU_USDA
	50	19.4	69.3	754	4	CB971008	CB971008 CAB10004_
	51	19.4	69.3	764	4	CB349108	CB349108 CAB2SG000
c	52	19.4	69.3	764	4	CB970930	CB970930 CAB10004_
	53	19.4	69.3	780	4	CB980281	CB980281 CAB70002_

	54	19.4	69.3	781	4	CA808979	CA808979 CA12LIO1I
	55	19.4	69.3	785	5	CF213737	CF213737 CGF100080
	56	19.4	69.3	787	5	CF208457	CF208457 CAB20003_
c	57	19.4	69.3	829	5	CF214167	CF214167 CGF100081
	58	19.4	69.3	839	4	CA818765	CA818765 CA12EI304
c	59	19.4	69.3	852	4	CB980342	CB980342 CAB70002_
	60	19.4	69.3	862	5	CF208465	CF208465 CAB20003_
	61	19.4	69.3	913	3	BQ797264	BQ797264 EST 6202
	62	19.2	68.6	122	9	DN776460	DN776460 E3963 [C5
c	63	19.2	68.6	171	2	BF842326	BF842326 PM0-HT107
c	64	19.2	68.6	202	2	BF842379	BF842379 PM0-HT107
c	65	19.2	68.6	212	2	BF842410	BF842410 PM0-HT107
c	66	19.2	68.6	605	8	CN107299	CN107299 EC2CAA30A
c	67	19.2	68.6	653	9	DN469148	DN469148 USDA-FP_1
	68	19.2	68.6	667	11	BZ317281	BZ317281 ib99h10.b
c	69	19.2	68.6	736	12	CE294405	CE294405 tigr-gss-
c	70	19.2	68.6	766	14	AG058271	AG058271 Pan trogl
c	71	19.2	68.6	808	11	BZ394306	BZ394306 EINBS27TF
	72	19.2	68.6	816	12	CC717843	CC717843 OGUKU30TV
	73	19.2	68.6	821	12	CC729085	CC729085 OGWET66TV
c	74	19.2	68.6	825	4	CA161837	CA161837 SCQGRZ301
c	75	19.2	68.6	879	13	CW962804	CW962804 AIAA-aaa2
	76	19.2	68.6	940	12	CG296976	CG296976 OG3BU83TH
	77	19.2	68.6	1101	14	CNS00FPE	AL070880 Drosophil
	78	19.2	68.6	1197	1	AM097523	AM097523 AM097523
	79	19	67.9	120	1	AL789777	AL789777 AL789777
c	80	19	67.9	301	10	T56569	T56569 yb34f12.r1
	81	19	67.9	318	7	AW094427	AW094427 EST287607
	82	19	67.9	332	1	AV259640	AV259640 AV259640
c	83	19	67.9	345	1	AL383611	AL383611 MtBC15E04
c	84	19	67.9	347	1	AL383612	AL383612 MtBC15E04
	85	19	67.9	404	2	BJ934619	BJ934619 BJ934619
	86	19	67.9	416	14	CT453068	CT453068 Sus scrof
	87	19	67.9	439	10	DT659787	DT659787 pgr1n.UA0
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	89	19	67.9	490	9	CX832786	CX832786 ACAC-aaa0
	90	19	67.9	494	5	CJ355644	CJ355644 CJ355644
c	91	19	67.9	523	9	CX572267	CX572267 TTE000218
c	92	19	67.9	524	1	AL366104	AL366104 MtBA04G08
	93	19	67.9	527	5	CK293095	CK293095 EST755809
c	94	19	67.9	527	7	BF514225	BF514225 UI-H-BW1-
	95	19	67.9	544	4	BW829082	BW829082 BW829082
c	96	19	67.9	553	10	DW573296	DW573296 EST_ssal_
	97	19	67.9	557	8	CV200481	CV200481 km04e08.y
c	98	19	67.9	573	12	CE155084	CE155084 tigr-gss-
c	99	19	67.9	577	14	DX203767	DX203767 OR_ABa007
	100	19	67.9	578	2	BJ558568	BJ558568 BJ558568
	101	19	67.9	595	14	DE013378	DE013378 Branchios
	102	19	67.9	596	10	DT280686	DT280686 JGI_CAAV9
	103	19	67.9	613	10	DR638765	DR638765 EST102939
	104	19	67.9	616	11	AZ605488	AZ605488 1M0426P18
	105	19	67.9	625	5	CD319894	CD319894 StrPu538.
	106	19	67.9	629	14	CR328767	CR328767 mte1-57N1
	107	19	67.9	643	14	CR865642	CR865642 Sus scrof
	108	19	67.9	645	2	BM489526	BM489526 pgm2n.pk0
	109	19	67.9	674	1	AJ392219	AJ392219 AJ392219
	110	19	67.9	680	8	CN227981	CN227981 RJB035F04
c	111	19	67.9	681	13	CW406721	CW406721 fsbb001f0
	112	19	67.9	681	14	DU749312	DU749312 HF10_110_
	113	19	67.9	684	13	CW163832	CW163832 104_571_1
c	114	19	67.9	690	13	CW210849	CW210849 104_641_1

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c 115      19   67.9    694   7   BF031627        BF031627 601558107
  116      19   67.9    706  14   DU837894         DU837894 MUGQ_CH25
c 117      19   67.9    707   9   CX577937        CX577937 TTE000321
c 118      19   67.9    708  11   BZ148827         BZ148827 CH230-395
  119      19   67.9    710   3   BU282966        BU282966 603863140
c 120      19   67.9    712  12   CG026493         CG026493 PGAAE71TF
  121      19   67.9    724  12   CL188575        CL188575 104_405_1
  122      19   67.9    725  10   DR614352         DR614352 EST100448
  123      19   67.9    758   9   CX617435        CX617435 GABR1_33_
  124      19   67.9    766  11   BZ181990         BZ181990 CH230-303
  125      19   67.9    768  14   CR149060         CR149060 Reverse s
  126      19   67.9    769  10   DR633644         DR633644 EST102426
  127      19   67.9    780  14   CR268915         CR268915 Reverse s
  128      19   67.9    783  14   CNS07BMA         AL438056 T7 end of
c 129      19   67.9    786   3   BQ150215        BQ150215 NF012G09L
  130      19   67.9    790  12   CG092006         CG092006 PUFKH44TD
  131      19   67.9    799  14   CR305599         CR305599 mte1-25I1
c 132      19   67.9    804   5   CJ445574        CJ445574 CJ445574
  133      19   67.9    806  14   AJ595292         AJ595292 Arabidops
  134      19   67.9    807  12   CC505625         CC505625 CH240_346
  135      19   67.9    808   4   BX078328        BX078328 BX078328
  136      19   67.9    810   4   BX079454        BX079454 BX079454
  137      19   67.9    812   4   CA920739        CA920739 EST638457
  138      19   67.9    812  12   CG197927         CG197927 PUFUS27TB
c 139      19   67.9    812  13   DU050592         DU050592 145226 To
c 140      19   67.9    814   8   CV289966        CV289966 aof01-11m
  141      19   67.9    817  12   CG228284         CG228284 OGVDX61TV
c 142      19   67.9    822  13   CZ953200         CZ953200 265024 To
c 143      19   67.9    824  11   B12075          B12075 F25H9-Sp6.2
  144      19   67.9    826   8   CO421648        CO421648 GGEZHT102
c 145      19   67.9    849  14   DU870776         DU870776 101855 To
  146      19   67.9    854   3   BU464015        BU464015 603773224
c 147      19   67.9    865   8   CV771138        CV771138 FGAS06553
c 148      19   67.9    880  13   CZ970396         CZ970396 174110 To
c 149      19   67.9    894  13   DU094231         DU094231 108916 To
  150      19   67.9    895   8   CV288139        CV288139 aof01-16m
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                              ALIGNMENTS


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RESULT 1
AG889518/c
LOCUS        AG889518              912 bp    DNA     linear   GSS 03-NOV-2004
DEFINITION   Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence,
             BAC clone:K0359C09_F, genomic survey sequence.
ACCESSION    AG889518
VERSION      AG889518.1  GI:55355779
KEYWORDS     GSS.
SOURCE       Oryza sativa (indica cultivar-group)
  ORGANISM   Oryza sativa (indica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
             clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1
  AUTHORS    Katagiri,S., Wu,J., Ito,Y., Karasawa,W., Shibata,M., Kanamori,H.,
             Katayose,Y., Namiki,N., Matsumoto,T. and Sasaki,T.
  TITLE      End Sequencing and Chromosomal in silico Mapping of BAC Clones
             Derived from an indica Rice Cultivar, Kasalath
  JOURNAL    Breeding Science 54, 273-279 (2004)
REFERENCE    2  (bases 1 to 912)
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SCORE Search Results Details for Application 1 630-536-2.rg

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:

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                       GenCore version 5.1.9
             Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 03:55:42 ; Search time 417.254 Seconds
                                          (without alignments)
                                          4291.222 Million cell updates/sec

Title:          US-10-630-536-2
Perfect score:  28
Sequence:       1 ccatgttcatgttatgtccaccaacaag 28

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
                10:  gb_vi:*
                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	28	100.0	28	2	CS001821	CS001821 Sequence
c	2	28	100.0	102	2	CS001823	CS001823 Sequence
c	3	28	100.0	2473	15	YPPFRATOX	X92727 Y.pestis to
c	4	28	100.0	96210	15	YPPMT1	AL117211 Yersinia
	5	28	100.0	100984	15	AF053947	AF053947 Yersinia
	6	28	100.0	100990	2	AR487637	AR487637 Sequence
	7	28	100.0	100990	15	AF074611	AF074611 Yersinia
c	8	28	100.0	106642	15	AE017045	AE017045 Yersinia
	9	28	100.0	137036	15	AJ698720	AJ698720 Yersinia
c	10	21.2	75.7	214978	12	AC182082	AC182082 Bos tauru
c	11	21.2	75.7	277211	12	AC164850	AC164850 Bos tauru
	12	20.6	73.6	3880	13	AY750997	AY750997 Anopheles
c	13	20.6	73.6	110000	4	AY661558_0	AY661558 Hordeum v
	14	20.6	73.6	138587	5	AC010363	AC010363 Homo sapi
c	15	20.6	73.6	143009	5	AC022447	AC022447 Homo sapi
	16	20.6	73.6	161076	5	HS272J12	Z82194 Human DNA s
c	17	20.6	73.6	200161	11	BX000431	BX000431 Zebrafish
c	18	20.6	73.6	250440	12	AC095968	AC095968 Rattus no
c	19	20.2	72.1	88087	12	AC110708	AC110708 Rattus no
	20	20.2	72.1	156589	5	HS537K23	AL034405 Human DNA
	21	20.2	72.1	233545	12	AC175307	AC175307 Bos tauru
c	22	20.2	72.1	251251	12	AC130500	AC130500 Rattus no
	23	20	71.4	589	7	BV356900	BV356900 S231P6154
	24	20	71.4	668	6	MMAJ5562	AJ005562 Mus Muscu
	25	20	71.4	680	6	AY158988	AY158988 Mus muscu
c	26	20	71.4	35641	12	AC014835	AC014835 Drosophil
	27	20	71.4	76748	12	AC014256	AC014256 Drosophil
c	28	20	71.4	90796	12	AP007405	AP007405 Lotus cor
	29	20	71.4	110000	4	AE017341_10	Continuation (11 o
	30	20	71.4	135774	12	AC091380	AC091380 Mus muscu
c	31	20	71.4	148847	13	AC008234	AC008234 Drosophil
	32	20	71.4	149793	6	AC129296	AC129296 Mus muscu
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c	34	20	71.4	165439	13	AC008215	AC008215 Drosophil
c	35	20	71.4	170403	13	AC008214	AC008214 Drosophil
	36	20	71.4	190168	6	AC127036	AC127036 Mus muscu
c	37	20	71.4	191834	13	AE003757	AE003757 Drosophil
c	38	20	71.4	224614	13	AE003682	AE003682 Drosophil
	39	20	71.4	280215	12	AC129648	AC129648 Rattus no
	40	19.8	70.7	1574	2	CQ574716	CQ574716 Sequence
	41	19.8	70.7	1679	13	AY058289	AY058289 Drosophil
c	42	19.8	70.7	4122	2	CQ574715	CQ574715 Sequence
	43	19.8	70.7	70496	12	AC017498	AC017498 Drosophil
c	44	19.8	70.7	81329	12	AC008300	AC008300 Drosophil
c	45	19.8	70.7	156346	13	AC006472	AC006472 Drosophil
	46	19.8	70.7	162995	6	AL663032	AL663032 Mouse DNA
c	47	19.8	70.7	186241	13	AC007086	AC007086 Drosophil
c	48	19.8	70.7	199271	12	AC142243	AC142243 Mus muscu
	49	19.8	70.7	297107	13	AE003833	AE003833 Drosophil
c	50	19.6	70.0	1769	5	AY599004S1	AY599004 Homo sapi
c	51	19.6	70.0	77850	5	AC080098	AC080098 Homo sapi
	52	19.6	70.0	92527	12	AC144962	AC144962 Xenopus t
	53	19.6	70.0	123000	6	AC098697	AC098697 Rattus no
c	54	19.6	70.0	128449	12	AC148508	AC148508 Carollia
	55	19.6	70.0	138589	5	AC092966	AC092966 Homo sapi
c	56	19.6	70.0	143714	5	AL390856	AL390856 Human DNA

	57	19.6	70.0	148846	12	AC176929	AC176929 Strongylo
	58	19.6	70.0	174622	6	AC079436	AC079436 Rattus no
	59	19.6	70.0	182891	12	AC025194	AC025194 Homo sapi
c	60	19.6	70.0	212066	12	AC180957	AC180957 Strongylo
c	61	19.6	70.0	230877	11	BX248500	BX248500 Zebrafish
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	63	19.6	70.0	232195	12	AC106493	AC106493 Rattus no
c	64	19.6	70.0	243184	12	AC103523	AC103523 Rattus no
c	65	19.6	70.0	265119	12	AC111373	AC111373 Rattus no
	66	19.6	70.0	276207	12	AC169661	AC169661 Bos tauru
	67	19.4	69.3	133093	6	AC134439	AC134439 Mus muscu
c	68	19.4	69.3	178416	6	AC140840	AC140840 Mus muscu
c	69	19.2	68.6	70102	12	AC180972	AC180972 Strongylo
c	70	19.2	68.6	77761	12	AP007340	AP007340 Lotus cor
c	71	19.2	68.6	108845	2	CQ869594	CQ869594 Sequence
	72	19.2	68.6	110000	4	CR380959_10	Continuation (11 o
	73	19.2	68.6	110000	4	AP008211_063	Continuation (64 o
	74	19.2	68.6	143966	4	AC135920	AC135920 Oryza sat
	75	19.2	68.6	154234	12	AC177086	AC177086 Strongylo
	76	19.2	68.6	161443	5	AC009884	AC009884 Homo sapi
	77	19.2	68.6	166862	5	CNS01DTS	AL132857 Human chr
c	78	19.2	68.6	167529	6	AC154773	AC154773 Mus muscu
c	79	19.2	68.6	172388	12	AC027634	AC027634 Homo sapi
	80	19.2	68.6	173707	12	AC172415	AC172415 Strongylo
	81	19.2	68.6	182583	12	AC177078	AC177078 Strongylo
c	82	19.2	68.6	183270	12	AC135532	AC135532 Rattus no
c	83	19.2	68.6	184939	12	AC160738	AC160738 Bos tauru
c	84	19.2	68.6	199891	5	CNS00M8O	AL079303 Human chr
	85	19.2	68.6	206059	11	AC148599	AC148599 Xenopus t
c	86	19.2	68.6	209284	12	AC107589	AC107589 Rattus no
	87	19.2	68.6	218539	12	AC171569	AC171569 Bos tauru
c	88	19.2	68.6	219066	12	AC172310	AC172310 Strongylo
	89	19.2	68.6	235586	12	AC098224	AC098224 Rattus no
c	90	19.2	68.6	243092	12	AC120099	AC120099 Rattus no
c	91	19	67.9	639	5	AF268418	AF268418 Homo sapi
c	92	19	67.9	643	5	BC059947	BC059947 Homo sapi
	93	19	67.9	687	11	AF292636	AF292636 Bothrops
	94	19	67.9	689	11	AY220340	AY220340 Atropoide
	95	19	67.9	689	11	AY220342	AY220342 Atropoide
	96	19	67.9	689	11	AY220343	AY220343 Atropoide
	97	19	67.9	689	11	AY220345	AY220345 Atropoide
	98	19	67.9	694	11	FAU49307	U49307 Farancia ab
	99	19	67.9	694	11	LMU41885	U41885 Lachesis mu
c	100	19	67.9	713	5	AF268420	AF268420 Homo sapi
c	101	19	67.9	750	2	BD215433	BD215433 Novel hum
c	102	19	67.9	750	2	AR769026	AR769026 Sequence
c	103	19	67.9	763	5	AF268421	AF268421 Homo sapi
	104	19	67.9	766	11	DQ098595	DQ098595 Pseudonaj
c	105	19	67.9	884	2	AR140640	AR140640 Sequence
c	106	19	67.9	884	2	BD140674	BD140674 Chondrosa
c	107	19	67.9	884	5	AF195880	AF195880 Homo sapi
c	108	19	67.9	1045	5	AF268419	AF268419 Homo sapi
c	109	19	67.9	2000	2	AX508649	AX508649 Sequence
	110	19	67.9	8858	12	AC014855	AC014855 Drosophil
c	111	19	67.9	40849	6	BX942826	BX942826 Mouse DNA
	112	19	67.9	42112	13	CBRG35L02	AC084559 Caenorhab
	113	19	67.9	55961	12	AC100947	AC100947 Mus muscu
	114	19	67.9	74166	12	AC151820	AC151820 Xenopus t
	115	19	67.9	84556	4	AC123571	AC123571 Medicago
	116	19	67.9	86797	12	AP008129	AP008129 Lotus cor
c	117	19	67.9	87072	5	AC078786	AC078786 Homo sapi

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   118      19   67.9  88709  12   AP007347              AP007347 Lotus cor
   119      19   67.9  88917   5   AL133226              AL133226 Human DNA
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ALIGNMENTS

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VERSION   CS001821.1 GI:58424076
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SOURCE   Yersinia pestis
  ORGANISM   Yersinia pestis
             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
             Enterobacteriaceae; Yersinia.
REFERENCE   1
  AUTHORS   McCready,P.M., Radnedge,L., Andersen,G.L., Ott,L.L., Slezak,T.R.,
             Kuczmarski,T.A. and Motin,V.L.
  TITLE   Nucleotide sequences specific to Yersinia pestis and methods for
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  JOURNAL   Patent: WO 2004106553-A 2 09-DEC-2004;
             The Regents of The University of California (US)
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SCORE Search Results Details for Application 10(
Result us-10-630-536-1.rng.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6.
start

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                        GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters:      10489840

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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-1.ı

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
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                    GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

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; Publication No. US20060123505A1
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;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
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;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK110933
;   DATABASE ENTRY DATE: 2001-12-06
```

SCORE Search Results Details for Application 10(and Search Result us-10-630-536-2.rng.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
start

```
                     GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 03:53:57 ; Search time 168.804 Seconds
                                           (without alignments)
                                           1156.508 Million cell updates/sec

Title:          US-10-630-536-2
Perfect score:  28
Sequence:       1 ccatgttcatgttatgtccaccaacaag 28

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:       10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      N_Geneseq_8:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

      Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	28	100.0	28	14	ADV04867	Adv04867 Yersinia
c	2	28	100.0	102	14	ADV04869	Adv04869 Yersinia
	3	28	100.0	100990	12	ADJ94407	Adj94407 Yersinia
c	4	20.6	73.6	1393	13	ADT17317	Adt17317 Plant cDN
c	5	20	71.4	262	12	ADP92382	Adp92382 Cotton ex
	6	19.8	70.7	1574	4	ABL03489	Abl03489 Drosophil
c	7	19.8	70.7	4122	4	ABL03488	Abl03488 Drosophil
	8	19.2	68.6	3175	5	AAS86513	Aas86513 DNA encod
c	9	19.2	68.6	108845	13	ABD32542	Abd32542 Mouse can
	10	19	67.9	597	12	ACH67060	Ach67060 Human gen
c	11	19	67.9	750	2	AAZ16105	Aaz16105 Human gen
c	12	19	67.9	884	2	AAZ06794	Aaz06794 CSA-1 (ch
c	13	19	67.9	2000	6	ABZ15539	Abz15539 Arabidops
c	14	19	67.9	302250	6	ABL67703	Abl67703 Oesophagu
c	15	18.6	66.4	819	4	ABL13317	Abl13317 Drosophil
	16	18.6	66.4	1203	3	AAC40476	Aac40476 Arabidops
c	17	18.6	66.4	1353	11	ACH97086	Ach97086 Klebsiell
c	18	18.6	66.4	2028	14	ADZ62330	Adz62330 Murine Fr
	19	18.6	66.4	2792	4	ABL14758	Abl14758 Drosophil
	20	18.6	66.4	2819	4	ABL13316	Abl13316 Drosophil
c	21	18.6	66.4	7844	14	ADZ45652	Adz45652 Human pap
c	22	18.4	65.7	619	13	ADQ79224	Adq79224 Novel can
c	23	18.4	65.7	900	1	AAN90842	Aan90842 Fragment
c	24	18.4	65.7	900	2	AAV62808	Aav62808 Tobacco P
c	25	18.4	65.7	900	2	AAV72992	Aav72992 PR-R majo
c	26	18.4	65.7	950	2	AAQ06184	Aaq06184 PR-R majo
c	27	18.4	65.7	1355	3	AAC47170	Aac47170 Arabidops
c	28	18.4	65.7	1355	15	AEF28559	Aef28559 Lead_Cere
c	29	18.4	65.7	1360	3	AAC48921	Aac48921 Arabidops
c	30	18.4	65.7	2103	10	ADF79382	Adf79382 Mouse Tol
	31	18.4	65.7	2608	10	ADB62903	Adb62903 Human cDN
c	32	18.4	65.7	8922	4	ABL04053	Abl04053 Drosophil
c	33	18.4	65.7	14552	4	ABL03818	Abl03818 Drosophil
	34	18.4	65.7	15913	4	ABL04052	Abl04052 Drosophil
	35	18.4	65.7	104514	11	ACN45168	Acn45168 Mouse gen
c	36	18.4	65.7	115050	14	ADZ12553	Adz12553 Murine ca
c	37	18.2	65.0	751	2	AAX99011	Aax99011 Human val
	38	18.2	65.0	1909	4	ABL29955	Abl29955 Drosophil
c	39	18.2	65.0	6048	4	ABL29954	Abl29954 Drosophil
c	40	18.2	65.0	39976	14	AED53818	Aed53818 Cosmid co
c	41	18.2	65.0	40962	4	ABL29926	Abl29926 Drosophil
c	42	18	64.3	118	12	ADL10947	Adl10947 Cat flea
	43	18	64.3	184	3	AAC10167	Aac10167 Human sec
	44	18	64.3	361	4	AAL00811	Aal00811 Human rep
c	45	18	64.3	390	11	ACH97745	Ach97745 Klebsiell
	46	18	64.3	581	3	AAZ29198	Aaz29198 Human mye
	47	18	64.3	581	6	ABN86591	Abn86591 Human pro
	48	18	64.3	715	4	AAF24648	Aaf24648 Fragment
	49	18	64.3	1031	12	ADM98676	Adm98676 HMG-CoA r
c	50	18	64.3	1599	13	ADT43542	Adt43542 Bacterial
c	51	18	64.3	1936	14	AEE49274	Aee49274 Human MET
	52	18	64.3	2091	11	ACL30309	Acl30309 Rice abio
	53	18	64.3	2166	11	ACL26045	Acl26045 Rice abio
	54	18	64.3	2620	8	ACF12882	Acf12882 Human cer
	55	18	64.3	2620	12	ADP21360	Adp21360 Gene KCNA
	56	18	64.3	3103	8	ACF12881	Acf12881 Human cer

	57	18	64.3	3103	12	ADF45471	Adf45471 Human vas
	58	18	64.3	3176	8	ACF12880	Acf12880 Human cer
	59	18	64.3	3176	10	ADE85678	Ade85678 Farnesyl
	60	18	64.3	3176	12	ADL70586	Adl70586 Cervical
c	61	18	64.3	3220	10	ADC26592	Adc26592 Human HMG
	62	18	64.3	3301	15	AEE83686	Aee83686 Human cDN
	63	18	64.3	3570	14	ADX25926	Adx25926 Novel cel
c	64	18	64.3	3629	2	AAQ91510	Aaq91510 Dextranas
	65	18	64.3	3779	4	ABL04090	Abl04090 Drosophil
	66	18	64.3	99500	6	AAD41740	Aad41740 Human REC
c	67	18	64.3	108359	9	ADA13316	Ada13316 Human fri
	68	18	64.3	110000	6	ABA90521_00	Aba90521 Genomic s
	69	18	64.3	110000	13	ABD32966_01	Continuation (2 of
c	70	18	64.3	164841	11	ACN44428	Acn44428 Mouse gen
	71	17.8	63.6	8473	14	ADV96538	Adv96538 Coronavir
	72	17.8	63.6	31233	14	ADV96543	Adv96543 Coronavir
	73	17.8	63.6	31357	14	ADV96541	Adv96541 Coronavir
	74	17.8	63.6	31357	14	ADV96542	Adv96542 Coronavir
	75	17.8	63.6	31357	15	AEF20938	Aef20938 Mouse gen
	76	17.6	62.9	190	4	AAI23601	Aai23601 Probe #13
	77	17.6	62.9	190	4	ABA68713	Aba68713 Human foe
	78	17.6	62.9	190	4	AAI48913	Aai48913 Probe #17
	79	17.6	62.9	190	4	ABA50744	Aba50744 Human bre
	80	17.6	62.9	190	4	ABA35677	Aba35677 Probe #14
	81	17.6	62.9	190	4	AAK42838	Aak42838 Human bon
	82	17.6	62.9	190	4	AAK17054	Aak17054 Human bra
	83	17.6	62.9	190	4	ABS42469	Abs42469 Human liv
	84	17.6	62.9	190	5	AAI09216	Aai09216 Probe #92
	85	17.6	62.9	190	6	ABS16893	Abs16893 Human gen
	86	17.6	62.9	245	12	ADO34646	Ado34646 Human SLI
c	87	17.6	62.9	454	13	ADX46463	Adx46463 Plant ful
	88	17.6	62.9	463	4	AAI14400	Aai14400 Probe #43
	89	17.6	62.9	463	4	ABA56127	Aba56127 Human foe
	90	17.6	62.9	463	4	AAI35773	Aai35773 Probe #44
	91	17.6	62.9	463	4	ABA45622	Aba45622 Human bre
	92	17.6	62.9	463	4	ABA25778	Aba25778 Probe #42
	93	17.6	62.9	463	4	AAK29811	Aak29811 Human bon
	94	17.6	62.9	463	4	AAK04315	Aak04315 Human bra
	95	17.6	62.9	463	4	ABS29459	Abs29459 Human liv
	96	17.6	62.9	463	5	AAI04223	Aai04223 Probe #42
	97	17.6	62.9	463	6	ABS04371	Abs04371 Human gen
c	98	17.6	62.9	660	6	ABN93342	Abn93342 Staphyloc
c	99	17.6	62.9	660	13	ADS04351	Ads04351 Staphyloc
c	100	17.6	62.9	685	8	ACA22764	Aca22764 Prokaryot
c	101	17.6	62.9	985	8	ACA22689	Aca22689 Prokaryot
	102	17.6	62.9	1479	14	ADW07606	Adw07606 GTase cDN
c	103	17.6	62.9	1807	3	AAC51305	Aac51305 Arabidops
c	104	17.6	62.9	1812	3	AAC39116	Aac39116 Arabidops
c	105	17.6	62.9	1963	10	ADG10825	Adg10825 Human STA
	106	17.6	62.9	2000	11	ACL38016	Acl38016 Rice stre
c	107	17.6	62.9	2496	13	ADX51760	Adx51760 Plant ful
c	108	17.6	62.9	2640	13	ADX49949	Adx49949 Plant ful
c	109	17.6	62.9	2737	13	ADX36444	Adx36444 Plant ful
	110	17.6	62.9	3182	4	AAH54683	Aah54683 S. epider
	111	17.6	62.9	3618	4	AAH54200	Aah54200 S. epider
c	112	17.6	62.9	4905	13	ADR23438	Adr23438 Fatty acy
c	113	17.6	62.9	5024	10	ADG10713	Adg10713 Human STA
c	114	17.6	62.9	5033	12	ADL12412	Adl12412 Human ste
c	115	17.6	62.9	5043	12	ADJ45488	Adj45488 cDNA enco
c	116	17.6	62.9	5043	12	ADP05440	Adp05440 Human ace
c	117	17.6	62.9	5043	12	ADQ79557	Adq79557 Human hep

```
c 118    17.6   62.9     5043  13  ADR25183          Adr25183 Breast ca
c 119    17.6   62.9     5043  13  ADR23436          Adr23436 Fatty acy
c 120    17.6   62.9     5043  13  ACF91619          Acf91619 Human SIR
c 121    17.6   62.9     5043  15  AEF74530          Aef74530 Human pol
c 122    17.6   62.9     5336  10  ADG10715          Adg10715 Human STA
c 123    17.6   62.9     5356   9  ACF04122        Acf04122 Human Fac
c 124    17.6   62.9     5356  13  ADR23437          Adr23437 Fatty acy
c 125    17.6   62.9     5356  13  ACF91620          Acf91620 Human SIR
c 126    17.6   62.9     5356  14  AED14396          Aed14396 Human cum
  127    17.6   62.9    10593  14  ACL64567          Acl64567 M. xanthu
  128    17.6   62.9    39159   4  ABL30024          Abl30024 Drosophil
c 129    17.6   62.9    39536   4  ABL15482          Abl15482 Drosophil
c 130    17.6   62.9    59359  11  ACN44220          Acn44220 Mouse gen
  131    17.6   62.9   110000  12  ADO34435_4        Continuation (5 of
  132    17.6   62.9   110000  12  ADO34435_5        Continuation (6 of
c 133    17.6   62.9   127432  12  ADO43653          Ado43653 Nucleotid
c 134    17.6   62.9   138941   8  ACC79695          Acc79695 Human tum
  135    17.4   62.1      114  12  ADL10463          Adl10463 Cat flea
  136    17.4   62.1      117  12  ADL11274          Adl11274 Cat flea
c 137    17.4   62.1      118   3  AAC94432          Aac94432 Cat flea
c 138    17.4   62.1      118  12  ADL11144          Adl11144 Cat flea
c 139    17.4   62.1      118  12  ADL11471          Adl11471 Cat flea
  140    17.4   62.1      118  12  ADL10038          Adl10038 Cat flea
c 141    17.4   62.1      118  12  ADL10921          Adl10921 Cat flea
  142    17.4   62.1      118  12  ADL11480          Adl11480 Cat flea
  143    17.4   62.1      118  12  ADL10804          Adl10804 Cat flea
c 144    17.4   62.1      118  12  ADL09955          Adl09955 Cat flea
  145    17.4   62.1      118  12  ADL10065          Adl10065 Cat flea
c 146    17.4   62.1      118  12  ADL11375          Adl11375 Cat flea
  147    17.4   62.1      118  12  ADL10089          Adl10089 Cat flea
c 148    17.4   62.1      118  12  ADL11037          Adl11037 Cat flea
  149    17.4   62.1      118  12  ADL11411          Adl11411 Cat flea
c 150    17.4   62.1      119  12  ADL10000          Adl10000 Cat flea
```

ALIGNMENTS

RESULT 1
ADV04867
ID   ADV04867 standard; DNA; 28 BP.
XX
AC   ADV04867;
XX
DT   24-FEB-2005   (first entry)
XX
DE   Yersinia pestis amplicon #1 reverse PCR primer.
XX
KW   Diagnosis; gene amplification; yersinia pestis infection; ss; PCR;
KW   primer.
XX
OS   Yersinia pestis.
XX
PN   WO2004106553-A2.
XX
PD   09-DEC-2004.
XX
PF   31-JUL-2003; 2003WO-US024135.
XX
PR   01-AUG-2002; 2002US-0400890P.
PR   29-JUL-2003; 2003US-00400890.

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-2.rn

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 536-2.rni.

start

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 04:28:37 ; Search time 34.3636 Seconds
                                         (without alignments)
                                         1524.607 Million cell updates/sec

Title:          US-10-630-536-2
Perfect score:  28
Sequence:       1 ccatgttcatgttatgtccaccaacaag 28

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:     2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      Issued_Patents_NA:*
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                3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result              Query
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	No.	Score	Match	Length	DB	ID	Description
	1	28	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
c	2	19	67.9	750	4	US-09-297-648-3575	Sequence 3575, Ap
c	3	19	67.9	884	3	US-09-042-225-3	Sequence 3, Appli
c	4	18.6	66.4	1353	3	US-09-489-039A-2881	Sequence 2881, Ap
c	5	18.4	65.7	441	3	US-09-270-767-4147	Sequence 4147, Ap
c	6	18.4	65.7	441	3	US-09-270-767-19429	Sequence 19429, A
c	7	18.4	65.7	798	3	US-09-248-796A-6709	Sequence 6709, Ap
c	8	18.4	65.7	900	2	US-08-181-271A-4	Sequence 4, Appli
c	9	18.4	65.7	900	2	US-08-449-315-4	Sequence 4, Appli
c	10	18.4	65.7	900	2	US-08-444-803-4	Sequence 4, Appli
c	11	18.4	65.7	900	2	US-08-449-043-4	Sequence 4, Appli
c	12	18.4	65.7	900	2	US-08-456-265A-4	Sequence 4, Appli
c	13	18.4	65.7	900	2	US-08-455-416-4	Sequence 4, Appli
c	14	18.4	65.7	900	2	US-08-455-244-4	Sequence 4, Appli
c	15	18.4	65.7	900	2	US-08-454-876-4	Sequence 4, Appli
c	16	18.4	65.7	900	2	US-08-457-364-4	Sequence 4, Appli
c	17	18.4	65.7	900	2	US-08-456-262-4	Sequence 4, Appli
c	18	18.4	65.7	900	2	US-08-456-240-4	Sequence 4, Appli
c	19	18.4	65.7	900	2	US-08-455-736-4	Sequence 4, Appli
c	20	18.4	65.7	900	2	US-08-971-217-4	Sequence 4, Appli
c	21	18.4	65.7	900	3	US-09-350-600-4	Sequence 4, Appli
c	22	18.4	65.7	900	3	US-09-906-234-4	Sequence 4, Appli
	23	18.4	65.7	1026	3	US-09-248-796A-472	Sequence 472, App
	24	18.4	65.7	2608	3	US-10-104-047-1057	Sequence 1057, Ap
c	25	18.4	65.7	45762	3	US-09-949-016-16651	Sequence 16651, A
c	26	18.4	65.7	85850	3	US-09-949-016-13424	Sequence 13424, A
	27	18.4	65.7	120727	3	US-09-949-016-15787	Sequence 15787, A
	28	18.4	65.7	120727	3	US-09-949-016-15788	Sequence 15788, A
	29	18	64.3	184	3	US-09-513-999C-14242	Sequence 14242, A
c	30	18	64.3	390	3	US-09-489-039A-3540	Sequence 3540, Ap
	31	18	64.3	601	3	US-09-949-016-109193	Sequence 109193,
	32	18	64.3	601	3	US-09-949-016-109194	Sequence 109194,
	33	18	64.3	601	3	US-09-949-016-109195	Sequence 109195,
	34	18	64.3	601	3	US-09-949-016-109196	Sequence 109196,
	35	18	64.3	601	3	US-09-949-016-122252	Sequence 122252,
c	36	18	64.3	3629	2	US-08-354-618-1	Sequence 1, Appli
	37	18	64.3	18556	3	US-09-949-016-15177	Sequence 15177, A
	38	18	64.3	23521	3	US-09-949-016-14592	Sequence 14592, A
	39	18	64.3	99500	3	US-09-798-096-10	Sequence 10, Appl
c	40	18	64.3	133278	3	US-09-949-016-12524	Sequence 12524, A
c	41	18	64.3	154600	3	US-09-949-016-14757	Sequence 14757, A
	42	17.6	62.9	483	3	US-09-621-976-17903	Sequence 17903, A
	43	17.6	62.9	601	3	US-09-949-016-109300	Sequence 109300,
	44	17.6	62.9	601	3	US-09-949-016-109301	Sequence 109301,
c	45	17.6	62.9	660	3	US-09-134-001C-2805	Sequence 2805, Ap
	46	17.6	62.9	1230	3	US-09-248-796A-1393	Sequence 1393, Ap
	47	17.6	62.9	3182	3	US-09-710-279-4047	Sequence 4047, Ap
	48	17.6	62.9	3618	3	US-09-710-279-3564	Sequence 3564, Ap
c	49	17.6	62.9	4943	3	US-09-949-016-1397	Sequence 1397, Ap
c	50	17.6	62.9	5033	3	US-09-976-594-141	Sequence 141, App
	51	17.6	62.9	10593	3	US-09-902-540-1030	Sequence 1030, Ap
c	52	17.6	62.9	88557	3	US-09-949-016-17028	Sequence 17028, A
c	53	17.6	62.9	95648	3	US-09-949-016-13139	Sequence 13139, A
	54	17.4	62.1	282	5	US-09-974-300-7739	Sequence 7739, Ap
c	55	17.4	62.1	288	3	US-09-134-001C-829	Sequence 829, App
c	56	17.4	62.1	601	3	US-09-949-016-87670	Sequence 87670, A
	57	17.4	62.1	627	3	US-09-328-352-1022	Sequence 1022, Ap
c	58	17.4	62.1	717	3	US-09-107-532A-1174	Sequence 1174, Ap
	59	17.4	62.1	1123	3	US-09-894-698-9	Sequence 9, Appli

c	60	17.4	62.1	1123	3	US-09-894-698-11	Sequence 11, Appl
	61	17.4	62.1	1123	3	US-10-180-165-9	Sequence 9, Appli
c	62	17.4	62.1	1123	3	US-10-180-165-11	Sequence 11, Appl
	63	17.4	62.1	1449	3	US-09-894-698-4	Sequence 4, Appli
c	64	17.4	62.1	1449	3	US-09-894-698-5	Sequence 5, Appli
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ALIGNMENTS

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; Patent No. 6706522
; GENERAL INFORMATION:
;   APPLICANT: Blattner, Frederick R.
;   APPLICANT: Burland, Valerie
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;   APPLICANT: Mayhew, George F.
;   APPLICANT: Perna, Nicole
;   APPLICANT: Perry, Robert D.
;   APPLICANT: Straley, Susan C.
;   APPLICANT: Fetherston, Jacqueline D.
;   APPLICANT: Lindler, Luther E.
;   APPLICANT: Plano, Gregory V.
;   TITLE OF INVENTION: Plasmid DNA From Yersinia Pestis
;   FILE REFERENCE: 960296.95939
;   CURRENT APPLICATION NUMBER: US/09/409,800B
;   CURRENT FILING DATE: 1999-09-30
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 100990
;   TYPE: DNA
;   ORGANISM: Yersinia pestis
US-09-409-800B-2

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-2.rn

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; APPLICANT: McCready, Paula M
; APPLICANT: Radnedge, Lyndsay
; APPLICANT: Anderson, Gary L.
; APPLICANT: Ott, Linda L.
; APPLICANT: Slezak, Thomas R.
; APPLICANT: Kuczmarski, Thomas A.
; APPLICANT: Motin, Vladimir L.
; TITLE OF INVENTION: Nucleotide Sequences Specific to Yersinia Pestis and Methods fo
; TITLE OF INVENTION: Detection of Yersinia Pestis
; FILE REFERENCE: IL-11030
; CURRENT APPLICATION NUMBER: US/10/630,536
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 24
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; Publication No. US20060134663A1
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; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
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               9:  gb_est8:*
               10:  gb_est9:*
               11:  gb_gss1:*
               12:  gb_gss2:*
               13:  gb_gss3:*
               14:  gb_gss4:*

     Pred. No. is the number of results predicted by chance to have a
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21.2	75.7	845	5	CJ425530	CJ425530 CJ425530
c	2	21.2	75.7	857	5	CJ416320	CJ416320 CJ416320
	3	20.6	73.6	391	7	BF145775	BF145775 WHE1840_E
	4	20.6	73.6	642	5	CD495560	CD495560 CDA17-C07
	5	20.6	73.6	708	10	DR625674	DR625674 EST101580
c	6	20.6	73.6	780	14	AG521832	AG521832 Mus muscu
c	7	20.6	73.6	791	12	CC409754	CC409754 PUHQQ21TD
c	8	20.6	73.6	846	12	BZ983753	BZ983753 PUFIT26TD
c	9	20.6	73.6	875	12	CG161555	CG161555 PUJFC77TD
	10	20.6	73.6	879	12	CC416414	CC416414 PUHPQ91TB
c	11	20.6	73.6	896	13	CZ303176	CZ303176 ZMMBF0080
	12	20.6	73.6	914	12	CC348780	CC348780 OGQAP55TH
c	13	20.6	73.6	928	12	CG281889	CG281889 OGZAV94TV
c	14	20.6	73.6	1020	12	CG384284	CG384284 OG3AI41TV
	15	20.6	73.6	1044	10	DW039689	DW039689 CFW285-D1
	16	20.2	72.1	704	12	CC625944	CC625944 OGWDV54TH
	17	20.2	72.1	763	12	CG066130	CG066130 PUFVJ48TB
	18	20.2	72.1	864	14	CT387691	CT387691 Sus scrof
c	19	20	71.4	356	3	BQ032746	BQ032746 UI-1-CF0-
	20	20	71.4	531	3	BP466503	BP466503 BP466503
	21	20	71.4	683	6	AK008778	AK008778 Mus muscu
	22	20	71.4	716	5	CF719176	CF719176 CCAGE17TF
	23	20	71.4	720	3	BP480490	BP480490 BP480490
	24	20	71.4	898	14	CT438237	CT438237 Sus scrof
c	25	19.8	70.7	740	7	AW940160	AW940160 GH04113.3
c	26	19.8	70.7	760	14	CNS00ABC	AL054959 Drosophil
c	27	19.6	70.0	295	4	BX634567	BX634567 BX634567
	28	19.6	70.0	310	1	AU260441	AU260441 AU260441
c	29	19.6	70.0	335	13	DU251887	DU251887 109853819
c	30	19.6	70.0	342	8	CN934020	CN934020 000202AVB
c	31	19.6	70.0	505	11	AQ618682	AQ618682 HS_5169_A
c	32	19.6	70.0	649	3	BU945308	BU945308 AGENCOURT
c	33	19.6	70.0	724	5	CK238795	CK238795 AGENCOURT
c	34	19.6	70.0	725	5	CJ411575	CJ411575 CJ411575
c	35	19.6	70.0	766	13	CZ598749	CZ598749 OM__Ba005
c	36	19.6	70.0	776	3	BU895388	BU895388 X023D06 P
c	37	19.6	70.0	776	5	CJ408652	CJ408652 CJ408652
	38	19.6	70.0	814	5	CJ427693	CJ427693 CJ427693
	39	19.6	70.0	825	12	CG074865	CG074865 PUJBV50TD
c	40	19.6	70.0	827	5	CJ416814	CJ416814 CJ416814
c	41	19.6	70.0	831	5	CJ414971	CJ414971 CJ414971
c	42	19.6	70.0	862	5	CJ418448	CJ418448 CJ418448
	43	19.6	70.0	879	5	CJ426032	CJ426032 CJ426032
	44	19.6	70.0	891	14	AG481185	AG481185 Mus muscu
	45	19.4	69.3	414	1	AI508053	AI508053 BSBmL3SZ0
	46	19.4	69.3	430	1	AA509301	AA509301 MBAFCX9F1
	47	19.4	69.3	443	1	AI076981	AI076981 BSBmMFSZ1
	48	19.4	69.3	522	1	AI043411	AI043411 BSBmMFSZ0
	49	19.4	69.3	568	1	AA257177	AA257177 SWMFCA146
	50	19.4	69.3	665	1	AA570887	AA570887 SWMFCA265
	51	19.4	69.3	740	7	AW561830	AW561830 KJBmL3SZ4
	52	19.4	69.3	780	1	AI939716	AI939716 BSBmMFSZ4
	53	19.4	69.3	1026	5	CD455832	CD455832 TNWbmfC19

c	54	19.4	69.3	1113	13	CL477743	CL477743 SAIL_279_
c	55	19.2	68.6	390	4	C05973	C05973 C05973 Huma
c	56	19.2	68.6	462	7	BE114187	BE114187 UI-R-CA0-
	57	19.2	68.6	485	11	AQ760183	AQ760183 HS_2026_A
	58	19.2	68.6	507	2	BJ525266	BJ525266 BJ525266
	59	19.2	68.6	559	10	DR459362	DR459362 CM075E04
c	60	19.2	68.6	564	12	CE732022	CE732022 tigr-gss-
	61	19.2	68.6	609	2	BJ527153	BJ527153 BJ527153
c	62	19.2	68.6	610	2	BJ537832	BJ537832 BJ537832
c	63	19.2	68.6	624	2	BJ539734	BJ539734 BJ539734
	64	19.2	68.6	657	5	CJ424160	CJ424160 CJ424160
c	65	19.2	68.6	725	12	CL178235	CL178235 104_386_1
c	66	19.2	68.6	744	10	DV701008	DV701008 CGN-47121
	67	19.2	68.6	765	12	CC531361	CC531361 CH240_408
c	68	19.2	68.6	778	8	CO222051	CO222051 WS01014.B
c	69	19.2	68.6	1019	13	CW931532	CW931532 EDCC845TF
	70	19.2	68.6	1037	4	BX399271	BX399271 BX399271
c	71	19.2	68.6	1248	13	CL644849	CL644849 CH213-82B
c	72	19.2	68.6	1258	14	AG278474	AG278474 Mus muscu
	73	19.2	68.6	1269	4	CB565516	CB565516 AGENCOURT
	74	19	67.9	162	7	AV912246	AV912246 AV912246
	75	19	67.9	233	3	BQ757128	BQ757128 EBem10_SQ
c	76	19	67.9	252	12	CL174910	CL174910 104_379_1
	77	19	67.9	276	7	AV777216	AV777216 AV777216
	78	19	67.9	287	14	AB156598	AB156598 Oryza sat
c	79	19	67.9	300	1	AJ461583	AJ461583 AJ461583
c	80	19	67.9	314	10	DV945298	DV945298 SB03002A1
	81	19	67.9	339	7	BF426863	BF426863 daa24a03.
c	82	19	67.9	349	11	AQ089263	AQ089263 HS_2208_A
	83	19	67.9	358	3	BP085655	BP085655 BP085655
c	84	19	67.9	383	2	BI336714	BI336714 AR080D08T
c	85	19	67.9	384	2	BG193951	BG193951 RST13092
	86	19	67.9	399	3	BP084757	BP084757 BP084757
	87	19	67.9	414	3	BQ660537	BQ660537 HI04B06u
	88	19	67.9	420	11	AZ250329	AZ250329 RPCI-23-4
	89	19	67.9	453	12	CC528454	CC528454 CH240_403
	90	19	67.9	477	13	CZ572588	CZ572588 OA_BBa014
	91	19	67.9	478	10	DT686603	DT686603 s13dFA39E
	92	19	67.9	480	1	AJ469356	AJ469356 AJ469356
	93	19	67.9	489	10	DT686819	DT686819 s13dFA33A
	94	19	67.9	489	13	CW115498	CW115498 104_490_1
	95	19	67.9	505	2	BM443605	BM443605 EBro02_SQ
	96	19	67.9	508	8	CN618864	CN618864 TgESTzyn1
	97	19	67.9	511	3	BP056169	BP056169 BP056169
c	98	19	67.9	512	8	CX308429	CX308429 C20009H03
c	99	19	67.9	513	8	CV892018	CV892018 4144280 B
	100	19	67.9	518	10	DT687666	DT687666 s13dFA22H
	101	19	67.9	520	10	DT687776	DT687776 s13dFA46E
	102	19	67.9	522	10	DT692834	DT692834 s13dFA19A
	103	19	67.9	530	10	DT688535	DT688535 s13dFA55C
	104	19	67.9	530	10	DW055469	DW055469 CLLX8004.
	105	19	67.9	533	2	BG040705	BG040705 NXSI_114_
	106	19	67.9	536	10	DT709955	DT709955 s13dFA47G
c	107	19	67.9	539	2	BM375607	BM375607 EBem06_SQ
	108	19	67.9	542	10	DT689354	DT689354 s13dFA07A
c	109	19	67.9	544	2	BG189235	BG189235 RST8279 A
	110	19	67.9	552	3	BQ663836	BQ663836 HU04E04u
	111	19	67.9	554	10	DT689245	DT689245 s13dFA34G
	112	19	67.9	554	10	DT690253	DT690253 s13dFA71A
	113	19	67.9	558	7	BF260357	BF260357 HVSMEf002
	114	19	67.9	564	10	DT672540	DT672540 s13dLT37G

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    115      19    67.9    569    3    BU993782           BU993782 HD14J15r
    116      19    67.9    569    9    DB155107           DB155107 DB155107
    117      19    67.9    578    2    BJ482027           BJ482027 BJ482027
    118      19    67.9    583    5    CF120697           CF120697 TgESTzyi3
c   119      19    67.9    584    2    BG212104           BG212104 RST31572
c   120      19    67.9    585    2    BI925759           BI925759 EST545648
c   121      19    67.9    591    2    BG524861           BG524861 8-39 Stev
c   122      19    67.9    594    3    BQ465642           BQ465642 HU04E04r
    123      19    67.9    594    3    BU999630           BU999630 HI15C15r
c   124      19    67.9    595   13    CW059671           CW059671 104_302_1
    125      19    67.9    601    3    BQ147300           BQ147300 NF038H06F
    126      19    67.9    606    2    BJ463811           BJ463811 BJ463811
    127      19    67.9    606   10    DT700345           DT700345 s13dFA29F
    128      19    67.9    610    7    AV940730           AV940730 AV940730
    129      19    67.9    611   10    DT708137           DT708137 s13dFA27C
c   130      19    67.9    612   10    DT707031           DT707031 s13dFA09H
    131      19    67.9    615   10    DT712983           DT712983 s13dFA19G
    132      19    67.9    616    4    CB860990           CB860990 HH03L24w
    133      19    67.9    621   10    DT670043           DT670043 s13dLT30F
c   134      19    67.9    624    6    CNS0A9BK           BX821982 Arabidops
    135      19    67.9    627   10    DT713664           DT713664 s13dFA32A
    136      19    67.9    630   10    DW072797           DW072797 CLLZ4204.
    137      19    67.9    631    2    BM443573           BM443573 EBro02_SQ
c   138      19    67.9    632    4    CA007979           CA007979 HU09I22r
    139      19    67.9    633   10    DW060231           DW060231 CLLY12767
    140      19    67.9    638   10    DW050751           DW050751 CLLX3537.
    141      19    67.9    641   10    DW072683           DW072683 CLLZ410.b
    142      19    67.9    642   10    DT711827           DT711827 s13dFA22D
    143      19    67.9    642   10    DW048821           DW048821 CLLX1567.
    144      19    67.9    642   10    DW050755           DW050755 CLLX3541.
    145      19    67.9    648    2    BI960398           BI960398 HVSMEn002
c   146      19    67.9    648   13    CL747853           CL747853 OR_BBa011
    147      19    67.9    649   10    DW069772           DW069772 CLLY9589.
    148      19    67.9    649   10    DW070831           DW070831 CLLZ2207.
c   149      19    67.9    650    2    BG711605           BG711605 pg11n.pk0
    150      19    67.9    651    5    CK450482           CK450482 900039 MA
```

ALIGNMENTS

RESULT 1
CJ425530
LOCUS   CJ425530   845 bp   mRNA   linear   EST 21-JUN-2005
DEFINITION   CJ425530 Molgula tectiformis unpublished cDNA library, larva
             Molgula tectiformis cDNA clone mtlv024d01 3', mRNA sequence.
ACCESSION   CJ425530
VERSION   CJ425530.1 GI:68118069
KEYWORDS   EST.
SOURCE   Molgula tectiformis
  ORGANISM   Molgula tectiformis
             Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
             Stolidobranchia; Molgulidae; Molgula.
REFERENCE   1 (bases 1 to 845)
  AUTHORS   Gyoja,F., Satou,Y. and Satoh,N.
  TITLE   Expressed genes in Molgula tectiformis
  JOURNAL   Unpublished (2005)
COMMENT   Contact: Tadasu Shin-i
             Center For Genetic Resource Information
             National Institute of Genetics
             1111 Yata, Mishima, Shizuoka 411-8540, Japan

SCORE Search Results Details for Application 10(
Search Result us-10-630-536-3.rng.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6.
start

```
                         GenCore version 5.1.9
               Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 03:53:57 ; Search time 198.947 Seconds
                                         (without alignments)
                                         1156.508 Million cell updates/sec

Title:          US-10-630-536-3
Perfect score:  33
Sequence:       1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      N_Geneseq_8:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
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                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
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                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	33	100.0	33	14	ADV04868	Adv04868 Yersinia
	2	33	100.0	102	14	ADV04869	Adv04869 Yersinia
c	3	33	100.0	100990	12	ADJ94407	Adj94407 Yersinia
	4	21.8	66.1	1722	10	ACF68430	Acf68430 Photorhab
	5	21.8	66.1	102644	10	ACF65378	Acf65378 Photorhab
	6	21.8	66.1	110000	10	ACF67367_11	Continuation (12 o
c	7	21.4	64.8	2081	12	ADP04087	Adp04087 Human col
	8	21	63.6	214019	10	ADL13809	Adl13809 Osteoarth
c	9	20.8	63.0	101169	12	ADQ97584	Adq97584 Mouse can
	10	20.6	62.4	161051	13	ABD32811	Abd32811 Human can
c	11	20.4	61.8	130263	6	ABK83573	Abk83573 Human cDN
c	12	20.2	61.2	1989	4	AAS03890	Aas03890 Human sec
	13	20.2	61.2	3093	12	ADP04510	Adp04510 Sea squir
c	14	20.2	61.2	52746	14	AEA61129	Aea61129 Human FLJ
c	15	20.2	61.2	74234	11	ACN44594	Acn44594 Human gen
	16	20.2	61.2	110000	11	ACN43998_3	Continuation (4 of
c	17	20	60.6	3638	4	ABL12764	Abl12764 Drosophil
	18	20	60.6	110000	14	AEE04876_6	Continuation (7 of
c	19	19.8	60.0	2669	12	ADO15889	Ado15889 4 synthes
c	20	19.8	60.0	29555	4	ABL18446	Abl18446 Drosophil
c	21	19.8	60.0	44748	11	ACN44064	Acn44064 Mouse gen
c	22	19.8	60.0	94330	11	ACN44662	Acn44662 Human gen
	23	19.8	60.0	116585	11	ACN43936	Acn43936 Mouse gen
c	24	19.8	60.0	209484	11	ACN44126	Acn44126 Human gen
c	25	19.6	59.4	313	13	ADU13837	Adu13837 Solid tum
c	26	19.6	59.4	3164	13	ADQ84812	Adq84812 Human tum
c	27	19.6	59.4	3164	13	ACN40700	Acn40700 Tumour-as
c	28	19.6	59.4	3188	6	ABL61777	Abl61777 Colon ade
c	29	19.6	59.4	3188	9	ACC85162	Acc85162 Human P13
c	30	19.6	59.4	3188	10	ADD29777	Add29777 Human tum
c	31	19.6	59.4	3190	2	AAZ11494	Aaz11494 Human pro
c	32	19.6	59.4	5173	4	ABL14096	Abl14096 Drosophil
c	33	19.4	58.8	852	2	AAX20460	Aax20460 Human sec
c	34	19.4	58.8	852	10	ADD90244	Add90244 Novel hum
c	35	19.4	58.8	852	10	ADG90063	Adg90063 Human cDN
c	36	19.4	58.8	852	14	ADY25403	Ady25403 Novel hum
c	37	19.4	58.8	1585	2	AAX97973	Aax97973 Human sec
c	38	19.4	58.8	1585	9	ADA11516	Ada11516 Human cDN
	39	19.4	58.8	2574	12	ADQ86023	Adq86023 Human tum
	40	19.4	58.8	2574	12	ADQ87487	Adq87487 Human tum
	41	19.4	58.8	2589	2	AAZ28760	Aaz28760 Human cyc
c	42	19.4	58.8	2775	11	ADM02633	Adm02633 Human cDN
c	43	19.4	58.8	2775	14	AEC85563	Aec85563 Human cDN
	44	19.4	58.8	3687	13	ADT05296	Adt05296 Haemophil
	45	19.4	58.8	3853	6	ABZ35020	Abz35020 Human gen
	46	19.4	58.8	3853	8	ACC50145	Acc50145 Breast ca
	47	19.4	58.8	3871	5	AAS87444	Aas87444 DNA encod
	48	19.4	58.8	4213	13	ADR07118	Adr07118 Full leng
	49	19.4	58.8	4863	14	AEB25798	Aeb25798 DNA encod
	50	19.4	58.8	4864	14	AEB25804	Aeb25804 DNA encod
	51	19.4	58.8	4864	14	AEB25802	Aeb25802 DNA encod
	52	19.4	58.8	4864	14	AEB25796	Aeb25796 DNA encod
	53	19.4	58.8	4864	14	AEB25800	Aeb25800 DNA encod
	54	19.4	58.8	4864	14	AEB25794	Aeb25794 DNA encod
	55	19.4	58.8	6147	8	ACC46453	Acc46453 Human dit
	56	19.4	58.8	9100	2	AAT28521	Aat28521 H. influe

	57	19.4	58.8	9100	4	ABA76851	Aba76851 Haemophil
c	58	19.4	58.8	110000	2	AAT42063_04	Continuation (5 of
c	59	19.4	58.8	110000	6	ABQ74964_5	Continuation (6 of
c	60	19.4	58.8	117576	13	ADT05736	Adt05736 Haemophil
	61	19.4	58.8	189013	8	ACF62741	Acf62741 Cancer ba
	62	19.4	58.8	189013	8	ADB20856	Adb20856 MRP1 base
	63	19.4	58.8	189013	10	ADB87945	Adb87945 Human UGT
	64	19.4	58.8	189013	10	ADB96928	Adb96928 Human MDR
	65	19.4	58.8	189013	10	ADB92119	Adb92119 Human MDR
	66	19.2	58.2	653	6	ABQ59694	Abq59694 Human col
c	67	19.2	58.2	731	8	ABZ20574	Abz20574 Cancer as
c	68	19.2	58.2	778	4	AAK63403	Aak63403 Human imm
c	69	19.2	58.2	778	4	AAK84849	Aak84849 Human imm
c	70	19.2	58.2	778	4	AAK84850	Aak84850 Human imm
	71	19.2	58.2	888	4	AAH01673	Aah01673 Microspor
c	72	19.2	58.2	1041	13	ADT05031	Adt05031 Haemophil
c	73	19.2	58.2	1437	13	ADO82662	Ado82662 Plant ful
c	74	19.2	58.2	1451	13	ADX49728	Adx49728 Plant ful
c	75	19.2	58.2	1528	13	ADX54310	Adx54310 Plant ful
	76	19.2	58.2	2785	4	ABL08936	Abl08936 Drosophil
	77	19.2	58.2	4362	4	ABL09880	Abl09880 Drosophil
	78	19.2	58.2	4842	12	ADN72188	Adn72188 Thale cre
c	79	19.2	58.2	13236	12	ADQ21058	Adq21058 Human sof
c	80	19.2	58.2	53981	11	ACN44928	Acn44928 Mouse gen
	81	19.2	58.2	78056	8	ABV99701	Abv99701 Bovine BS
	82	19.2	58.2	78056	15	AEE20443	Aee20443 Bovine pr
c	83	19.2	58.2	170170	10	ADL13643	Adl13643 Osteoarth
	84	19.2	58.2	191996	13	ADT05647	Adt05647 Haemophil
c	85	19.2	58.2	217409	11	ACN45150	Acn45150 Human gen
c	86	19	57.6	492	5	ABA14023	Aba14023 Human ner
	87	19	57.6	2513	12	ADQ67417	Adq67417 Novel hum
c	88	19	57.6	32183	4	AAS35994	Aas35994 Human car
c	89	19	57.6	32183	10	ADE46688	Ade46688 Human car
c	90	19	57.6	32183	13	ADJ08106	Adj08106 Human car
	91	19	57.6	32190	5	AAS29937	Aas29937 Human lun
	92	19	57.6	32190	10	ADB33274	Adb33274 Human nov
	93	19	57.6	32193	5	AAS29936	Aas29936 Human lun
	94	19	57.6	32193	10	ADB33273	Adb33273 Human nov
	95	19	57.6	51558	13	ACN37207	Acn37207 Human per
	96	19	57.6	51935	4	AAK75883	Aak75883 Human imm
	97	19	57.6	110000	6	ABA03041_25	Continuation (26 o
	98	19	57.6	118951	8	ABT17385	Abt17385 Human IG
c	99	18.8	57.0	121	12	ADK92706	Adk92706 Polynucle
c	100	18.8	57.0	201	13	ADS39739	Ads39739 Human aut
	101	18.8	57.0	245	2	AAT09778	Aat09778 Tomato ge
	102	18.8	57.0	314	3	AAC28325	Aac28325 Human sec
	103	18.8	57.0	363	5	ADI68108	Adi68108 Human ova
	104	18.8	57.0	363	5	ADI74480	Adi74480 Human ova
	105	18.8	57.0	374	5	AAF67183	Aaf67183 Novel hum
	106	18.8	57.0	380	5	AAF67191	Aaf67191 Novel hum
	107	18.8	57.0	380	11	ACN87001	Acn87001 Breast ca
	108	18.8	57.0	396	4	AAL11455	Aal11455 Human bre
	109	18.8	57.0	411	5	ADL39717	Adl39717 Human ova
	110	18.8	57.0	416	9	ACH47499	Ach47499 Human inf
	111	18.8	57.0	430	4	AAL20354	Aal20354 Human bre
c	112	18.8	57.0	454	2	AAX83400	Aax83400 Breast ca
c	113	18.8	57.0	454	2	AAV68935	Aav68935 DNA molec
c	114	18.8	57.0	454	3	AAC80923	Aac80923 Human bre
c	115	18.8	57.0	454	6	AAS99769	Aas99769 Breast tu
c	116	18.8	57.0	454	6	ABK46813	Abk46813 Human bre
c	117	18.8	57.0	454	8	ADA11290	Ada11290 Human bre

```
c 118     18.8     57.0     454    10   ADC15263              Adc15263 Human bre
  119     18.8     57.0     541    11   ACN81656              Acn81656 Breast ca
  120     18.8     57.0     567    13   ACN48276              Acn48276 Cotton pr
c 121     18.8     57.0     583     7   ADS72103              Ads72103 Human kid
c 122     18.8     57.0     583     7   ADW40957              Adw40957 cDNA elev
  123     18.8     57.0     599     9   ACH27358              Ach27358 Human adu
  124     18.8     57.0     615     6   ABK92240              Abk92240 Prostate
  125     18.8     57.0     634     6   AAS99871              Aas99871 Breast tu
  126     18.8     57.0     634     8   ADA11406              Ada11406 Human bre
  127     18.8     57.0     634    10   ADC15379              Adc15379 Human bre
  128     18.8     57.0     641    10   ABT21894              Abt21894 Breast ca
  129     18.8     57.0     687     9   ADB83179              Adb83179 Human cDN
  130     18.8     57.0     687    12   ADQ22655              Adq22655 Human sof
  131     18.8     57.0     695     9   ADB82602              Adb82602 Human cDN
  132     18.8     57.0     735     5   AAS76643              Aas76643 DNA encod
  133     18.8     57.0     768     6   ABQ89662              Abq89662 Human pro
  134     18.8     57.0     808    13   ADP55689              Adp55689 Human PRO
  135     18.8     57.0     874     9   ADB83260              Adb83260 Human cDN
  136     18.8     57.0     876    10   ADC15394              Adc15394 Human bre
  137     18.8     57.0     876    10   ADC15393              Adc15393 Human bre
  138     18.8     57.0     879     3   AAC81016              Aac81016 Human bre
  139     18.8     57.0     879     4   AAH93826              Aah93826 Human pro
  140     18.8     57.0     879     4   AAI94008              Aai94008 Human neu
  141     18.8     57.0     879     4   AAS63919              Aas63919 Human pro
  142     18.8     57.0     879     4   AAH85140              Aah85140 Human pro
  143     18.8     57.0     879     5   ACA59727              Aca59727 Prostate
  144     18.8     57.0     879     6   ABL95290              Abl95290 Human B30
  145     18.8     57.0     879     6   AAS99862              Aas99862 Breast tu
  146     18.8     57.0     879     8   ACC95454              Acc95454 Prostate
  147     18.8     57.0     879     8   ADA11393              Ada11393 Human bre
  148     18.8     57.0     879    10   ADC15366              Adc15366 Human bre
  149     18.8     57.0     879    10   ADB13981              Adb13981 Human pro
  150     18.8     57.0     879    10   ADG26397              Adg26397 Human pro
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ALIGNMENTS

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RESULT 1
ADV04868
ID    ADV04868 standard; DNA; 33 BP.
XX
AC    ADV04868;
XX
DT    24-FEB-2005  (first entry)
XX
DE    Yersinia pestis amplicon #1 probe.
XX
KW    Diagnosis; gene amplification; yersinia pestis infection; ss; probe.
XX
OS    Yersinia pestis.
XX
PN    WO2004106553-A2.
XX
PD    09-DEC-2004.
XX
PF    31-JUL-2003; 2003WO-US024135.
XX
PR    01-AUG-2002; 2002US-0400890P.
PR    29-JUL-2003; 2003US-00400890.
XX
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SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-3.r

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 3.rni.

start

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                         GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 04:28:37 ; Search time 40.5 Seconds
                                          (without alignments)
                                          1524.607 Million cell updates/sec

Title:          US-10-630-536-3
Perfect score:  33
Sequence:       1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      Issued_Patents_NA:*
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                6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
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                8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

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c    1       33    100.0  100990  3   US-09-409-800B-2        Sequence 2, Appli
c    2       20     60.6  390416  3   US-09-949-016-16923     Sequence 16923, A
c    3     19.8     60.0     601  3   US-09-949-016-33518     Sequence 33518, A
c    4     19.8     60.0     601  3   US-09-949-016-60370     Sequence 60370, A
     5     19.8     60.0     601  3   US-09-949-016-149247    Sequence 149247,
     6     19.8     60.0    1127  3   US-09-270-767-14416     Sequence 14416, A
     7     19.8     60.0   47347  3   US-09-949-016-14130     Sequence 14130, A
     8     19.8     60.0   49721  3   US-09-949-016-17538     Sequence 17538, A
c    9     19.8     60.0  128516  3   US-09-949-016-13501     Sequence 13501, A
c   10     19.8     60.0  133157  3   US-09-949-016-12541     Sequence 12541, A
c   11     19.8     60.0  187169  3   US-09-949-016-12776     Sequence 12776, A
c   12     19.8     60.0  191569  3   US-09-949-016-15940     Sequence 15940, A
    13     19.4     58.8    2589  2   US-08-482-728A-3        Sequence 3, Appli
    14     19.4     58.8    9100  2   US-08-743-637B-27       Sequence 27, Appl
    15     19.4     58.8    9100  3   US-08-526-840B-27       Sequence 27, Appl
c   16     19.4     58.8  117838  3   US-09-949-016-17595     Sequence 17595, A
c   17     19.4     58.8  786431  3   US-09-751-389-3         Sequence 3, Appli
c   18     19.4     58.8 1830121  3   US-09-557-884-1         Sequence 1, Appli
c   19     19.4     58.8 1830121  3   US-09-643-990A-1        Sequence 1, Appli
c   20     19.4     58.8 1830121  3   US-10-158-865-1         Sequence 1, Appli
    21     19.2     58.2     601  3   US-09-949-016-96617     Sequence 96617, A
    22     19.2     58.2     601  3   US-09-949-016-96618     Sequence 96618, A
    23     19.2     58.2     601  3   US-09-949-016-96883     Sequence 96883, A
    24     19.2     58.2     601  3   US-09-949-016-96884     Sequence 96884, A
    25     19.2     58.2     601  3   US-09-949-016-97149     Sequence 97149, A
    26     19.2     58.2     601  3   US-09-949-016-97150     Sequence 97150, A
    27     19.2     58.2     601  3   US-09-949-016-97415     Sequence 97415, A
    28     19.2     58.2     601  3   US-09-949-016-97416     Sequence 97416, A
    29     19.2     58.2     601  3   US-09-949-016-97681     Sequence 97681, A
    30     19.2     58.2     601  3   US-09-949-016-97682     Sequence 97682, A
    31     19.2     58.2     601  3   US-09-949-016-97947     Sequence 97947, A
    32     19.2     58.2     601  3   US-09-949-016-97948     Sequence 97948, A
    33     19.2     58.2     601  3   US-09-949-016-98213     Sequence 98213, A
    34     19.2     58.2     601  3   US-09-949-016-98214     Sequence 98214, A
    35     19.2     58.2     601  3   US-09-949-016-98479     Sequence 98479, A
    36     19.2     58.2     601  3   US-09-949-016-98480     Sequence 98480, A
    37     19.2     58.2     601  3   US-09-949-016-98745     Sequence 98745, A
    38     19.2     58.2     601  3   US-09-949-016-98746     Sequence 98746, A
    39     19.2     58.2     601  3   US-09-949-016-99011     Sequence 99011, A
    40     19.2     58.2     601  3   US-09-949-016-99012     Sequence 99012, A
    41     19.2     58.2     601  3   US-09-949-016-99277     Sequence 99277, A
    42     19.2     58.2     601  3   US-09-949-016-99278     Sequence 99278, A
    43     19.2     58.2     601  3   US-09-949-016-99543     Sequence 99543, A
    44     19.2     58.2     601  3   US-09-949-016-99544     Sequence 99544, A
    45     19.2     58.2     601  3   US-09-949-016-99809     Sequence 99809, A
    46     19.2     58.2     601  3   US-09-949-016-99810     Sequence 99810, A
    47     19.2     58.2     601  3   US-09-949-016-100075    Sequence 100075,
    48     19.2     58.2     601  3   US-09-949-016-100076    Sequence 100076,
    49     19.2     58.2     601  3   US-09-949-016-100341    Sequence 100341,
    50     19.2     58.2     601  3   US-09-949-016-100342    Sequence 100342,
    51     19.2     58.2     601  3   US-09-949-016-100607    Sequence 100607,
    52     19.2     58.2     601  3   US-09-949-016-100608    Sequence 100608,
    53     19.2     58.2     601  3   US-09-949-016-100873    Sequence 100873,
    54     19.2     58.2     601  3   US-09-949-016-100874    Sequence 100874,
    55     19.2     58.2     601  3   US-09-949-016-100929    Sequence 100929,
    56     19.2     58.2     601  3   US-09-949-016-100930    Sequence 100930,
    57     19.2     58.2     601  3   US-09-949-016-101177    Sequence 101177,
    58     19.2     58.2     601  3   US-09-949-016-101178    Sequence 101178,
    59     19.2     58.2     601  3   US-09-949-016-101443    Sequence 101443,
    60     19.2     58.2     601  3   US-09-949-016-101444    Sequence 101444,
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SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-3.rnpbm.

| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-3.rnpbm.

start

Go Back to previous pa

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:38:10 ; Search time 459.395 Seconds
                                          (without alignments)
                                          882.666 Million cell updates/sec

Title:           US-10-630-536-3
Perfect score:   33
Sequence:        1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       Published_Applications_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	33	100.0	102	11	US-10-630-536-4	Sequence 4, Appli
c	3	22.4	67.9	598	12	US-10-301-480-454944	Sequence 454944,
c	4	22.4	67.9	598	12	US-10-301-480-454945	Sequence 454945,
c	5	22.4	67.9	598	12	US-10-301-480-454946	Sequence 454946,
c	6	22.4	67.9	598	12	US-10-301-480-1068353	Sequence 1068353,
c	7	22.4	67.9	598	12	US-10-301-480-1068354	Sequence 1068354,
c	8	22.4	67.9	598	12	US-10-301-480-1068355	Sequence 1068355,
c	9	22.4	67.9	620	4	US-09-925-065A-386363	Sequence 386363,
c	10	22.4	67.9	620	4	US-09-925-065A-386364	Sequence 386364,
c	11	22.4	67.9	620	4	US-09-925-065A-386365	Sequence 386365,
c	12	22.4	67.9	620	5	US-09-925-065A-386363	Sequence 386363,
c	13	22.4	67.9	620	5	US-09-925-065A-386364	Sequence 386364,
c	14	22.4	67.9	620	5	US-09-925-065A-386365	Sequence 386365,
c	15	22	66.7	598	12	US-10-301-480-454943	Sequence 454943,
c	16	22	66.7	598	12	US-10-301-480-1068352	Sequence 1068352,
c	17	22	66.7	620	4	US-09-925-065A-386362	Sequence 386362,
c	18	22	66.7	620	5	US-09-925-065A-386362	Sequence 386362,
c	19	20.8	63.0	1672	10	US-10-750-185-35124	Sequence 35124, A
c	20	20.8	63.0	1672	10	US-10-750-623-35124	Sequence 35124, A
c	21	20.8	63.0	85506	7	US-10-085-117-220	Sequence 220, App
c	22	20.8	63.0	101169	11	US-10-330-773-561	Sequence 561, App
	23	20.6	62.4	161051	9	US-10-417-375-170	Sequence 170, App
	24	20.4	61.8	600	10	US-10-972-079-90890	Sequence 90890, A
	25	20.4	61.8	600	10	US-10-972-079-90891	Sequence 90891, A
	26	20.4	61.8	600	10	US-10-972-079-90892	Sequence 90892, A
	27	20.4	61.8	600	10	US-10-972-079-90893	Sequence 90893, A
	28	20.4	61.8	761	6	US-10-027-632-33780	Sequence 33780, A
	29	20.4	61.8	761	6	US-10-027-632-33781	Sequence 33781, A
	30	20.4	61.8	761	7	US-10-027-632-33780	Sequence 33780, A
	31	20.4	61.8	761	7	US-10-027-632-33781	Sequence 33781, A
	32	20.4	61.8	1663	4	US-09-925-065A-723444	Sequence 723444,
	33	20.4	61.8	1663	5	US-09-925-065A-723444	Sequence 723444,
	34	20.2	61.2	271	4	US-09-925-065A-524709	Sequence 524709,
	35	20.2	61.2	271	4	US-09-925-065A-524710	Sequence 524710,
	36	20.2	61.2	271	5	US-09-925-065A-524709	Sequence 524709,
	37	20.2	61.2	271	5	US-09-925-065A-524710	Sequence 524710,
	38	20.2	61.2	514	4	US-09-925-065A-260898	Sequence 260898,
	39	20.2	61.2	514	5	US-09-925-065A-260898	Sequence 260898,
	40	20.2	61.2	525	12	US-10-301-480-339238	Sequence 339238,
	41	20.2	61.2	525	12	US-10-301-480-952647	Sequence 952647,
c	42	20.2	61.2	574	4	US-09-925-065A-269821	Sequence 269821,
c	43	20.2	61.2	574	5	US-09-925-065A-269821	Sequence 269821,
c	44	20.2	61.2	579	12	US-10-301-480-347363	Sequence 347363,
c	45	20.2	61.2	579	12	US-10-301-480-960772	Sequence 960772,
	46	20.2	61.2	586	4	US-09-925-065A-608330	Sequence 608330,
	47	20.2	61.2	586	4	US-09-925-065A-608331	Sequence 608331,
	48	20.2	61.2	586	4	US-09-925-065A-608332	Sequence 608332,
	49	20.2	61.2	586	4	US-09-925-065A-608333	Sequence 608333,
	50	20.2	61.2	586	5	US-09-925-065A-608330	Sequence 608330,
	51	20.2	61.2	586	5	US-09-925-065A-608331	Sequence 608331,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-3.rnpbn.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-3.rnpbn.

start

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                      GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:39:12 ; Search time 34.2632 Seconds
                                           (without alignments)
                                           1138.902 Million cell updates/sec

Title:           US-10-630-536-3
Perfect score:   33
Sequence:        1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters:      1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       Published_Applications_NA_New:*
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                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                      %
Result                Query
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	No.	Score	Match	Length	DB	ID	Description
c	1	20.8	63.0	1548	7	US-11-266-748A-180468	Sequence 180468,
	2	20.8	63.0	1548	7	US-11-266-748A-240706	Sequence 240706,
c	3	20.4	61.8	130263	7	US-11-266-748A-58551	Sequence 58551, A
	4	19.8	60.0	385	7	US-11-266-748A-252438	Sequence 252438,
c	5	19.8	60.0	385	7	US-11-266-748A-312955	Sequence 312955,
c	6	19.8	60.0	597	7	US-11-266-748A-267118	Sequence 267118,
c	7	19.8	60.0	597	7	US-11-266-748A-280557	Sequence 280557,
	8	19.8	60.0	597	7	US-11-266-748A-327635	Sequence 327635,
c	9	19.8	60.0	421987	7	US-11-266-748A-28210	Sequence 28210, A
c	10	19.6	59.4	387	7	US-11-266-748A-178565	Sequence 178565,
c	11	19.6	59.4	415	7	US-11-266-748A-4042	Sequence 4042, Ap
c	12	19.6	59.4	879	7	US-11-266-748A-41287	Sequence 41287, A
c	13	19.6	59.4	1000	7	US-11-266-748A-116706	Sequence 116706,
	14	19.6	59.4	1000	7	US-11-266-748A-158870	Sequence 158870,
c	15	19.6	59.4	1000	7	US-11-266-748A-221937	Sequence 221937,
c	16	19.6	59.4	1000	7	US-11-266-748A-287513	Sequence 287513,
	17	19.6	59.4	1000	7	US-11-266-748A-338942	Sequence 338942,
c	18	19.6	59.4	1000	7	US-11-266-748A-398227	Sequence 398227,
	19	19.6	59.4	1000	7	US-11-266-748A-469273	Sequence 469273,
c	20	19.6	59.4	1118	7	US-11-266-748A-69120	Sequence 69120, A
	21	19.6	59.4	1118	7	US-11-266-748A-121931	Sequence 121931,
c	22	19.6	59.4	1478	7	US-11-266-748A-251523	Sequence 251523,
c	23	19.6	59.4	1478	7	US-11-266-748A-275484	Sequence 275484,
	24	19.6	59.4	1478	7	US-11-266-748A-312040	Sequence 312040,
c	25	19.6	59.4	3158	7	US-11-266-748A-31538	Sequence 31538, A
c	26	19.6	59.4	3204	7	US-11-266-748A-31537	Sequence 31537, A
c	27	19.6	59.4	3241	7	US-11-266-748A-29773	Sequence 29773, A
c	28	19.4	58.8	555	7	US-11-266-748A-168573	Sequence 168573,
c	29	19.4	58.8	893	7	US-11-266-748A-182628	Sequence 182628,
	30	19.4	58.8	976	7	US-11-266-748A-356698	Sequence 356698,
c	31	19.4	58.8	976	7	US-11-266-748A-440077	Sequence 440077,
	32	19.4	58.8	1618	7	US-11-266-748A-93308	Sequence 93308, A
c	33	19.4	58.8	1618	7	US-11-266-748A-146119	Sequence 146119,
c	34	19.4	58.8	2081	7	US-11-266-748A-186932	Sequence 186932,
	35	19.4	58.8	2081	7	US-11-266-748A-241617	Sequence 241617,
c	36	19.4	58.8	2775	7	US-11-293-697-1318	Sequence 1318, Ap
	37	19.4	58.8	3853	7	US-11-302-033-1	Sequence 1, Appli
	38	19.4	58.8	3853	7	US-11-266-748A-28964	Sequence 28964, A
c	39	19.2	58.2	932	6	US-10-953-349-18568	Sequence 18568, A
c	40	19.2	58.2	1449	6	US-10-953-349-13505	Sequence 13505, A
	41	19.2	58.2	1480	6	US-10-953-349-21936	Sequence 21936, A
c	42	19.2	58.2	2089	6	US-10-449-902-10155	Sequence 10155, A
c	43	19.2	58.2	4006	6	US-10-449-902-28263	Sequence 28263, A
	44	19.2	58.2	200033	7	US-11-266-748A-23936	Sequence 23936, A
c	45	19	57.6	417	7	US-11-266-748A-360929	Sequence 360929,
	46	19	57.6	417	7	US-11-266-748A-444308	Sequence 444308,
	47	19	57.6	131546	7	US-11-266-748A-60109	Sequence 60109, A
c	48	18.8	57.0	387	7	US-11-266-748A-36485	Sequence 36485, A
	49	18.8	57.0	653	7	US-11-266-748A-49300	Sequence 49300, A
c	50	18.8	57.0	780	7	US-11-217-529-77764	Sequence 77764, A
	51	18.8	57.0	822	7	US-11-266-748A-55221	Sequence 55221, A
c	52	18.8	57.0	864	7	US-11-266-748A-1000	Sequence 1000, Ap
	53	18.8	57.0	864	7	US-11-266-748A-62726	Sequence 62726, A
c	54	18.8	57.0	864	7	US-11-266-748A-65558	Sequence 65558, A
	55	18.8	57.0	875	7	US-11-266-748A-165742	Sequence 165742,
	56	18.8	57.0	1006	6	US-10-525-126-108	Sequence 108, App
	57	18.8	57.0	1079	7	US-11-266-748A-186067	Sequence 186067,
	58	18.8	57.0	1079	7	US-11-266-748A-193429	Sequence 193429,
c	59	18.8	57.0	1079	7	US-11-266-748A-241205	Sequence 241205,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-3.rst.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-3.rst.

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Go Back to previous page

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:17:07 ; Search time 1197.08 Seconds
                                           (without alignments)
                                           1541.534 Million cell updates/sec

Title:           US-10-630-536-3
Perfect score:   33
Sequence:        1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       EST:*
                 1:   gb_est1:*
                 2:   gb_est3:*
                 3:   gb_est4:*
                 4:   gb_est5:*
                 5:   gb_est6:*
                 6:   gb_htc:*
                 7:   gb_est2:*
                 8:   gb_est7:*
                 9:   gb_est8:*
                 10:  gb_est9:*
                 11:  gb_gss1:*
                 12:  gb_gss2:*
                 13:  gb_gss3:*
                 14:  gb_gss4:*

       Pred. No. is the number of results predicted by chance to have a
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23	69.7	644	14	CR029088	CR029088 Reverse s
c	2	23	69.7	741	14	CR210450	CR210450 Reverse s
	3	22.6	68.5	1076	12	CC232438	CC232438 CH261-153
c	4	22.4	67.9	610	3	BU479093	BU479093 603470978
	5	22.4	67.9	755	14	AG495577	AG495577 Mus muscu
	6	22	66.7	584	3	BP529535	BP529535 BP529535
	7	21.8	66.1	323	11	BZ212891	BZ212891 CH230-342
	8	21.8	66.1	535	13	CZ204066	CZ204066 AIAA-aae1
	9	21.8	66.1	699	14	CT093861	CT093861 Sus scrof
	10	21.8	66.1	719	14	CT152488	CT152488 Sus scrof
	11	21.8	66.1	740	14	AG162543	AG162543 Pan trogl
	12	21.8	66.1	915	14	DU517106	DU517106 109860981
	13	21.6	65.5	595	11	AQ880712	AQ880712 HS_5055_B
c	14	21.6	65.5	658	8	CN949960	CN949960 Ha_mx0_27
c	15	21.6	65.5	904	12	CG813163	CG813163 SOYDA36TV
c	16	21.4	64.8	542	13	DU284843	DU284843 109844829
c	17	21.4	64.8	609	14	CT150101	CT150101 Sus scrof
c	18	21.4	64.8	663	4	BX507342	BX507342 DKFZp779E
	19	21.4	64.8	1101	14	CNS00FW1	AL071321 Drosophil
	20	21.2	64.2	547	1	AA472123	AA472123 vh10d04.r
	21	21.2	64.2	547	10	DT902166	DT902166 mgsn0402
	22	21.2	64.2	547	10	DT908521	DT908521 mgsn0401
	23	21.2	64.2	617	2	BG077133	BG077133 H3011B12-
c	24	21.2	64.2	696	14	DU529868	DU529868 109860994
	25	21.2	64.2	872	4	CB203027	CB203027 AGENCOURT
	26	21.2	64.2	3409	6	AK034075	AK034075 Mus muscu
	27	21	63.6	493	7	BF041073	BF041073 BP250009B
c	28	21	63.6	564	14	CR205643	CR205643 Reverse s
	29	21	63.6	663	4	BY746719	BY746719 BY746719
c	30	21	63.6	730	14	AG075415	AG075415 Pan trogl
c	31	21	63.6	765	12	BZ774479	BZ774479 mcv95f02.
	32	21	63.6	786	9	DN043441	DN043441 JGI_CABA2
c	33	21	63.6	936	14	CNS03EE0	AL240273 Tetraodon
c	34	21	63.6	1006	13	CW958942	CW958942 TcB54.4_G
	35	20.8	63.0	251	5	CD933887	CD933887 GR45.122E
	36	20.8	63.0	325	11	AQ361021	AQ361021 HS_5034_B
c	37	20.8	63.0	421	2	BF987726	BF987726 QV0-GN014
	38	20.8	63.0	456	12	CC888070	CC888070 SALK_1512
	39	20.8	63.0	459	4	CB075617	CB075617 hz49c03.b
	40	20.8	63.0	473	7	BE165959	BE165959 MR3-HT048
c	41	20.8	63.0	473	11	AQ407551	AQ407551 HS_5097_B
	42	20.8	63.0	475	8	CV030602	CV030602 9773 Full
c	43	20.8	63.0	480	5	CJ139390	CJ139390 CJ139390
	44	20.8	63.0	493	11	AZ289232	AZ289232 RPCI-23-5
c	45	20.8	63.0	520	4	BW552416	BW552416 BW552416
c	46	20.8	63.0	532	2	BI705970	BI705970 fp98f11.y
c	47	20.8	63.0	532	4	BW568160	BW568160 BW568160
	48	20.8	63.0	537	9	DB214916	DB214916 DB214916
	49	20.8	63.0	538	11	BH737892	BH737892 BOMLA27TR
c	50	20.8	63.0	547	9	DA380460	DA380460 DA380460
c	51	20.8	63.0	556	4	BW584091	BW584091 BW584091
c	52	20.8	63.0	560	4	BW554235	BW554235 BW554235
c	53	20.8	63.0	569	12	CE685767	CE685767 tigr-gss-

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-4.rge.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-4.rge.

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                     GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 03:55:42 ; Search time 1520 Seconds
                                          (without alignments)
                                          4291.222 Million cell updates/sec

Title:          US-10-630-536-4
Perfect score:  102
Sequence:       1 atttcccaccaatcaacgat..........tggacataacatgaacatgg 102

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:       12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
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                8:  gb_sy:*
                9:  gb_un:*
                10:  gb_vi:*
                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	102	100.0	102	2	CS001823	CS001823 Sequence
	2	102	100.0	2473	15	YPPFRATOX	X92727 Y.pestis to
	3	102	100.0	96210	15	YPPMT1	AL117211 Yersinia
c	4	102	100.0	100984	15	AF053947	AF053947 Yersinia
c	5	102	100.0	100990	2	AR487637	AR487637 Sequence
c	6	102	100.0	100990	15	AF074611	AF074611 Yersinia
	7	102	100.0	106642	15	AE017045	AE017045 Yersinia
c	8	102	100.0	137036	15	AJ698720	AJ698720 Yersinia
	9	52.4	51.4	102644	2	AX770900	AX770900 Sequence
c	10	52.4	51.4	348813	15	BX571865	BX571865 Photorhab
c	11	34.4	33.7	266486	12	AC173090	AC173090 Bos tauru
	12	34	33.3	185906	12	CR678384	CR678384 Danio rer
c	13	34	33.3	205171	12	CR354612	CR354612 Danio rer
	14	34	33.3	222684	12	CT027629	CT027629 Danio rer
	15	34	33.3	229567	12	CR394539	CR394539 Danio rer
	16	33.8	33.1	189371	12	AC023125	AC023125 Homo sapi
c	17	33.8	33.1	191772	5	AC022825	AC022825 Homo sapi
	18	33	32.4	33	2	CS001822	CS001822 Sequence
	19	32.8	32.2	178091	12	AC110894	AC110894 Mus muscu
c	20	32.8	32.2	217077	6	AC153876	AC153876 Mus muscu
c	21	32.2	31.6	7053	13	DDIDIRS1A	M11339 Slime mold
	22	32.2	31.6	224334	12	AC096041	AC096041 Rattus no
	23	31.8	31.2	286	2	AR251962	AR251962 Sequence
	24	31.8	31.2	157843	12	AC046139	AC046139 Homo sapi
	25	31.8	31.2	166014	12	AC026080	AC026080 Homo sapi
	26	31.8	31.2	166452	5	AC092954	AC092954 Homo sapi
	27	31.6	31.0	25699	12	AC167633	AC167633 Bos tauru
c	28	31.6	31.0	84464	5	HS782D21	AL022399 Human DNA
	29	31.6	31.0	280112	12	AC098963	AC098963 Rattus no
c	30	31.4	30.8	187625	12	AC129257	AC129257 Rattus no
	31	31.4	30.8	193989	5	AC015743	AC015743 Homo sapi
	32	31.2	30.6	110000	12	AC107372_0	AC107372 Mus muscu
c	33	31.2	30.6	110000	12	AC118203_0	AC118203 Mus muscu
c	34	31.2	30.6	157057	12	AC127160	AC127160 Rattus no
	35	31.2	30.6	178748	12	AC141955	AC141955 Rattus no
c	36	31.2	30.6	202231	6	AL772407	AL772407 Mouse DNA
c	37	31.2	30.6	220013	12	AC108622	AC108622 Rattus no
	38	31.2	30.6	247670	12	AC117025	AC117025 Rattus no
	39	31	30.4	471	2	CQ699243	CQ699243 Sequence
c	40	31	30.4	31099	13	CEK03A11	Z77133 Caenorhabdi
c	41	31	30.4	84759	12	AP000730	AP000730 Homo sapi
c	42	31	30.4	135581	12	AP000771	AP000771 Homo sapi
	43	31	30.4	167306	5	AP001877	AP001877 Homo sapi
	44	31	30.4	240412	12	AC114078	AC114078 Rattus no
c	45	30.8	30.2	824	7	BV509807	BV509807 qxa86h06.
	46	30.8	30.2	37049	15	MLACEA	Z46257 M.leprae ac
	47	30.8	30.2	77170	12	AC018532	AC018532 Homo sapi
	48	30.8	30.2	93495	12	AC177979	AC177979 Strongylo
c	49	30.8	30.2	142215	5	BS000165	BS000165 Pan trogl
	50	30.8	30.2	145449	12	AC179396	AC179396 Strongylo
	51	30.8	30.2	147160	12	AC181723	AC181723 Strongylo
c	52	30.8	30.2	154896	12	AC110481	AC110481 Rattus no

c	53	30.8	30.2	185533	6	AC158389	AC158389 Mus muscu
c	54	30.8	30.2	197310	11	BX957253	BX957253 Zebrafish
c	55	30.8	30.2	199577	12	AC125873	AC125873 Rattus no
c	56	30.8	30.2	206088	12	CR944667	CR944667 Danio rer
	57	30.8	30.2	209968	12	AC125872	AC125872 Rattus no
c	58	30.8	30.2	213683	12	CR356230	CR356230 Danio rer
c	59	30.8	30.2	250128	12	AC162246	AC162246 Bos tauru
	60	30.8	30.2	250627	12	AC097031	AC097031 Rattus no
	61	30.8	30.2	251288	12	AC097593	AC097593 Rattus no
	62	30.8	30.2	342300	15	MLEPRTN8	AL583924 Mycobacte
c	63	30.6	30.0	4576	13	DDIDIRS1B	M11340 Slime mold
c	64	30.6	30.0	70640	12	AC149527	AC149527 Xenopus t
c	65	30.6	30.0	90373	13	AC115680	AC115680 Dictyoste
c	66	30.6	30.0	141396	11	BX005047	BX005047 Zebrafish
	67	30.6	30.0	150805	11	CR388021	CR388021 Zebrafish
c	68	30.6	30.0	151719	5	CNS05TET	AL359333 Human chr
	69	30.6	30.0	168905	6	AC129975	AC129975 Mus muscu
c	70	30.6	30.0	175009	5	CNS05TEY	AL359680 Human chr
	71	30.6	30.0	176054	6	AC134324	AC134324 Mus muscu
	72	30.6	30.0	191668	6	AC151968	AC151968 Mus muscu
	73	30.6	30.0	204945	6	AC167564	AC167564 Mus muscu
c	74	30.6	30.0	227182	11	BX005355	BX005355 Zebrafish
	75	30.4	29.8	127220	12	AC178924	AC178924 Strongylo
c	76	30.4	29.8	155593	12	AC179775	AC179775 Strongylo
	77	30.4	29.8	226802	12	CR392337	CR392337 Danio rer
	78	30.4	29.8	227706	11	BX571720	BX571720 Zebrafish
c	79	30.4	29.8	252593	12	AC112434	AC112434 Rattus no
c	80	30.2	29.6	42377	5	AL358152	AL358152 Human DNA
	81	30.2	29.6	78579	12	AC177634	AC177634 Strongylo
c	82	30.2	29.6	109101	12	AC177095	AC177095 Strongylo
	83	30.2	29.6	110000	15	AE015929_17	Continuation (18 o
	84	30.2	29.6	110000	15	CP000029_17	Continuation (18 o
	85	30.2	29.6	118875	6	AL928541	AL928541 Mouse DNA
	86	30.2	29.6	125944	12	AC177545	AC177545 Strongylo
c	87	30.2	29.6	129172	12	AC177623	AC177623 Strongylo
c	88	30.2	29.6	149765	5	AC004984	AC004984 Homo sapi
	89	30.2	29.6	168247	12	AC073025	AC073025 Homo sapi
	90	30.2	29.6	182201	12	AC176207	AC176207 Strongylo
c	91	30.2	29.6	188716	11	AL807739	AL807739 Zebrafish
	92	30.2	29.6	195937	5	AC096762	AC096762 Homo sapi
c	93	30.2	29.6	204896	12	AC125809	AC125809 Rattus no
	94	30.2	29.6	270897	12	AC096415	AC096415 Rattus no
c	95	30	29.4	378	4	AJ865281	AJ865281 Cocos nuc
	96	30	29.4	652	7	BV432809	BV432809 S237P6430
c	97	30	29.4	130057	5	AL357912	AL357912 Human DNA
	98	30	29.4	161405	12	AC120449	AC120449 Rattus no
	99	30	29.4	180438	6	AC117748	AC117748 Mus muscu
	100	29.8	29.2	1385	13	AY204177	AY204177 Caenorhab
	101	29.8	29.2	42271	12	TANN4_18	Continuation (19 o
	102	29.8	29.2	110000	12	TANN4_17	Continuation (18 o
	103	29.8	29.2	110000	15	BA000016_10	Continuation (11 o
c	104	29.8	29.2	117577	4	CR962126	CR962126 Medicago
c	105	29.8	29.2	124721	12	AC177318	AC177318 Strongylo
	106	29.8	29.2	127487	4	CT033769	CT033769 Medicago
c	107	29.8	29.2	144570	12	AC132990	AC132990 Rattus no
c	108	29.8	29.2	148793	6	AC116898	AC116898 Mus muscu
	109	29.8	29.2	150343	6	AC127355	AC127355 Mus muscu
	110	29.8	29.2	157171	12	AC155454	AC155454 Zea mays
c	111	29.8	29.2	180809	12	AC138275	AC138275 Mus muscu
	112	29.8	29.2	212410	12	AC118804	AC118804 Rattus no
c	113	29.8	29.2	222195	11	BX465868	BX465868 Zebrafish

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c 114    29.8   29.2 233458   12   AC132561          AC132561 Rattus no
  115    29.6   29.0   1843    4   AB122081          AB122081 Viburnum
c 116    29.6   29.0  36307   12   AY714849          AY714849 Unculture
c 117    29.6   29.0  93582    5   AC090681          AC090681 Homo sapi
c 118    29.6   29.0  98734    4   AC002333          AC002333 Arabidops
  119    29.6   29.0 110000   15   AJ938182_09       Continuation (10 o
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c 121    29.6   29.0 110000   15   AP008934_20       Continuation (21 o
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  125    29.6   29.0 151465   12   AC117371          AC117371 Homo sapi
  126    29.6   29.0 154608   12   AC073620          AC073620 Homo sapi
  127    29.6   29.0 155849    6   BX572626          BX572626 Mouse DNA
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c 129    29.6   29.0 219116   12   AC170978          AC170978 Bos tauru
  130    29.6   29.0 225968   12   AC112843          AC112843 Rattus no
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  137    29.4   28.8   1585    4   MTR299399         AJ299399 Medicago
c 138    29.4   28.8   1707    4   BT015922          BT015922 Arabidops
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  140    29.4   28.8   2979    4   AY115842          AY115842 Medicago
c 141    29.4   28.8   3611   11   BC077560          BC077560 Xenopus 1
c 142    29.4   28.8   9787   12   AC014416          AC014416 Drosophil
c 143    29.4   28.8  99284    5   AL662905          AL662905 Human DNA
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c 146    29.4   28.8 110000   13   CP000224_0        CP000224 Drosophil
c 147    29.4   28.8 110000   13   CP000224_1        Continuation (2 of
c 148    29.4   28.8 118507    4   ATF7J8            AL137189 Arabidops
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                              ALIGNMENTS


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DEFINITION    Sequence 4 from Patent WO2004106553.
ACCESSION     CS001823
VERSION       CS001823.1  GI:58424078
KEYWORDS      .
SOURCE        Yersinia pestis
  ORGANISM    Yersinia pestis
              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
              Enterobacteriaceae; Yersinia.
REFERENCE     1
  AUTHORS     McCready,P.M., Radnedge,L., Andersen,G.L., Ott,L.L., Slezak,T.R.,
              Kuczmarski,T.A. and Motin,V.L.
  TITLE       Nucleotide sequences specific to Yersinia pestis and methods for
              the detection of Yersinia pestis
  JOURNAL     Patent: WO 2004106553-A 4 09-DEC-2004;
              The Regents of The University of California (US)
FEATURES             Location/Qualifiers
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SCORE Search Results Details for Application 10
10-630-536-1.rge.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:

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                        GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 03:55:42 ; Search time 417.254 Seconds
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                Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:      12732272

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Post-processing: Minimum Match 0%
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	8	28	100.0	106642	15	AE017045	AE017045 Yersinia
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	12	21.2	75.7	37727	4	SPBC19G7	AL021839 S.pombe c
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	14	20.6	73.6	84798	12	AP007827	AP007827 Lotus cor
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	16	20.6	73.6	110000	15	CP000127_02	Continuation (3 of
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c	21	20.2	72.1	162605	12	AC068698	AC068698 Homo sapi
	22	20.2	72.1	164275	5	AC005157	AC005157 Homo sapi
c	23	20.2	72.1	192092	6	AC126248	AC126248 Mus muscu
c	24	20	71.4	816	4	AK110933	AK110933 Oryza sat
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	37	20	71.4	143969	5	AL357552	AL357552 Human DNA
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c	41	20	71.4	167525	12	BX890543	BX890543 Danio rer
	42	20	71.4	167663	12	AC158454	AC158454 Dasypus n
	43	20	71.4	168108	5	AC104119	AC104119 Homo sapi
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SCORE Search Results Details for Application 10(
Search Result us-10-630-536-4.rng.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
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                        GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

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	9	30.2	29.6	1488	6	ABN91973	Abn91973 Staphyloc
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	22	28.4	27.8	1482	10	ADD52523	Add52523 Staphyloc
	23	28.4	27.8	1509	6	ABA51669	Aba51669 Staphyloc
	24	28.4	27.8	1509	10	ADC21401	Adc21401 Staphyloc
	25	28.4	27.8	1509	10	ADC25087	Adc25087 DNA encod
	26	28.4	27.8	1509	10	ADD52589	Add52589 Staphyloc
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	45	27.6	27.1	1704	8	ACA18618	Aca18618 Prokaryot
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	56	27.2	26.7	2677	4	ABL21388	Abl21388 Drosophil

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-4.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 4.rni.

start

Go Back to pre·

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                        GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        July  1, 2006, 04:28:37 ; Search time 125.182 Seconds
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                        %
Result              Query
   No.    Score  Match Length DB   ID                      Description
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c   1     102   100.0  100990    3   US-09-409-800B-2        Sequence 2, Appli
    2    31.8    31.2     286    3   US-09-313-294A-7321     Sequence 7321, Ap
    3    30.2    29.6    1488    3   US-09-134-001C-1436     Sequence 1436, Ap
c   4    29.6    29.0   72504    3   US-09-949-016-14855     Sequence 14855, A
c   5    28.8    28.2     601    3   US-09-949-016-84207     Sequence 84207, A
c   6    28.6    28.0    9062    3   US-08-956-171E-85       Sequence 85, Appl
c   7    28.6    28.0    9062    3   US-08-781-986A-85       Sequence 85, Appl
    8    28.6    28.0   15817    3   US-09-949-016-16496     Sequence 16496, A
c   9    28.6    28.0  251672    3   US-09-949-016-17296     Sequence 17296, A
c  10    28.6    28.0  251682    3   US-09-949-016-11973     Sequence 11973, A
   11    28.4    27.8    1183    3   US-08-956-171E-476      Sequence 476, App
   12    28.4    27.8    1183    3   US-08-781-986A-476      Sequence 476, App
   13    28.4    27.8    1482    3   US-09-828-523A-21       Sequence 21, Appl
   14    28.4    27.8    1509    3   US-09-828-523A-89       Sequence 89, Appl
   15      28    27.5    3310    3   US-09-710-279-4143      Sequence 4143, Ap
c  16      28    27.5   25973    3   US-09-949-016-14140     Sequence 14140, A
   17    27.8    27.3     433    3   US-09-437-450A-38       Sequence 38, Appl
c  18    27.6    27.1     601    3   US-09-949-016-84206     Sequence 84206, A
   19    27.6    27.1    1368    3   US-09-614-221A-284      Sequence 284, App
   20    27.6    27.1    1704    3   US-09-711-164-238       Sequence 238, App
   21    27.6    27.1    4740    3   US-09-487-558B-367      Sequence 367, App
   22    27.6    27.1  117391    3   US-09-949-016-13945     Sequence 13945, A
c  23    27.6    27.1  455726    3   US-09-949-016-14157     Sequence 14157, A
c  24    27.6    27.1  481115    3   US-09-949-016-11940     Sequence 11940, A
c  25    27.2    26.7     601    3   US-09-949-002-3629      Sequence 3629, Ap
c  26    27.2    26.7     601    3   US-09-949-002-3630      Sequence 3630, Ap
c  27    27.2    26.7     601    3   US-09-949-002-5474      Sequence 5474, Ap
c  28    27.2    26.7     601    3   US-09-949-002-5475      Sequence 5475, Ap
   29    27.2    26.7    1116    3   US-09-248-796A-3645     Sequence 3645, Ap
   30    27.2    26.7   10190    3   US-10-232-858-105       Sequence 105, App
   31    27.2    26.7   10190    3   US-09-338-063A-105      Sequence 105, App
c  32    27.2    26.7   59158    3   US-09-949-002-728       Sequence 728, App
c  33    27.2    26.7   64994    3   US-09-949-002-688       Sequence 688, App
c  34    27.2    26.7   75929    3   US-09-949-016-15543     Sequence 15543, A
c  35    27.2    26.7   75929    3   US-09-949-016-15544     Sequence 15544, A
c  36      27    26.5  113876    3   US-09-949-016-14828     Sequence 14828, A
c  37      27    26.5  113876    3   US-09-949-016-14829     Sequence 14829, A
c  38      27    26.5  115508    3   US-09-949-016-11800     Sequence 11800, A
c  39      27    26.5  115508    3   US-09-949-016-14826     Sequence 14826, A
c  40      27    26.5  115508    3   US-09-949-016-14827     Sequence 14827, A
   41    26.8    26.3   66109    4   US-09-880-107-3768      Sequence 3768, Ap
   42    26.8    26.3  198285    4   US-09-880-107-3814      Sequence 3814, Ap
   43    26.8    26.3  199471    3   US-09-949-016-14083     Sequence 14083, A
c  44    26.8    26.3 1830121    3    US-09-557-884-1        Sequence 1, Appli
c  45    26.8    26.3 1830121    3    US-09-643-990A-1       Sequence 1, Appli
c  46    26.8    26.3 1830121    3    US-10-158-865-1        Sequence 1, Appli
   47    26.6    26.1    3015    3   US-09-134-000C-2014     Sequence 2014, Ap
   48    26.4    25.9     528    5   US-09-974-300-6115      Sequence 6115, Ap
   49    26.4    25.9     582    5   US-09-974-300-6100      Sequence 6100, Ap
c  50    26.4    25.9    1501    3   US-09-774-528-231       Sequence 231, App
c  51    26.4    25.9    1501    3   US-10-120-988-231       Sequence 231, App
   52    26.4    25.9    1602    3   US-09-134-001C-1216     Sequence 1216, Ap
c  53    26.4    25.9   32392    3   US-09-662-254B-27       Sequence 27, Appl
   54    26.4    25.9   95750    3   US-09-949-016-11926     Sequence 11926, A
   55    26.2    25.7    1644    3   US-09-248-796A-2122     Sequence 2122, Ap
   56      26    25.5     601    3   US-09-949-016-38426     Sequence 38426, A
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   58      26    25.5     601    3   US-09-949-016-176231    Sequence 176231,
   59      26    25.5     601    3   US-09-949-016-176269    Sequence 176269,
   60      26    25.5     601    3   US-09-949-016-176307    Sequence 176307,
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SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-4.rnpbm.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
4.rnpbm.

start

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                        GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:38:10 ; Search time 1419.95 Seconds
                                           (without alignments)
                                           882.666 Million cell updates/sec

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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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	3	31.8	31.2	550	4	US-09-925-065A-116209	Sequence 116209,
	4	31.8	31.2	550	5	US-09-925-065A-116209	Sequence 116209,
	5	31.8	31.2	555	12	US-10-301-480-215091	Sequence 215091,
	6	31.8	31.2	555	12	US-10-301-480-828500	Sequence 828500,
c	7	31.4	30.8	617	4	US-09-925-065A-482222	Sequence 482222,
c	8	31.4	30.8	617	4	US-09-925-065A-482223	Sequence 482223,
c	9	31.4	30.8	617	4	US-09-925-065A-482224	Sequence 482224,
c	10	31.4	30.8	617	5	US-09-925-065A-482222	Sequence 482222,
c	11	31.4	30.8	617	5	US-09-925-065A-482223	Sequence 482223,
c	12	31.4	30.8	617	5	US-09-925-065A-482224	Sequence 482224,
	13	31.4	30.8	618	4	US-09-925-065A-486061	Sequence 486061,
	14	31.4	30.8	618	5	US-09-925-065A-486061	Sequence 486061,
	15	31.2	30.6	1428	8	US-10-425-114-4532	Sequence 4532, Ap
	16	31	30.4	471	8	US-10-242-535A-44169	Sequence 44169, A
	17	31	30.4	471	8	US-10-085-783A-44169	Sequence 44169, A
	18	30.6	30.0	541	6	US-10-027-632-42175	Sequence 42175, A
	19	30.6	30.0	541	7	US-10-027-632-42175	Sequence 42175, A
	20	30.2	29.6	1488	8	US-10-724-972A-82	Sequence 82, Appl
	21	29.6	29.0	2162	9	US-10-425-115-55632	Sequence 55632, A
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c	23	29	28.4	777	5	US-09-925-065A-932706	Sequence 932706,
	24	29	28.4	1670	8	US-10-425-114-8757	Sequence 8757, Ap
	25	29	28.4	1676	8	US-10-425-114-11385	Sequence 11385, A
	26	29	28.4	1678	8	US-10-425-114-10929	Sequence 10929, A
	27	29	28.4	2991	8	US-10-424-599-120243	Sequence 120243,
c	28	28.8	28.2	201	9	US-10-719-993-13830	Sequence 13830, A
	29	28.8	28.2	520	6	US-10-027-632-282317	Sequence 282317,
	30	28.8	28.2	520	7	US-10-027-632-282317	Sequence 282317,
	31	28.6	28.0	192	9	US-10-674-124A-1114	Sequence 1114, Ap
	32	28.6	28.0	579	6	US-10-027-632-34442	Sequence 34442, A
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c	35	28.6	28.0	9062	8	US-10-329-624-85	Sequence 85, Appl
	36	28.6	28.0	43009	6	US-10-087-192-1582	Sequence 1582, Ap
	37	28.6	28.0	184868	15	US-11-121-086-88	Sequence 88, Appl
c	38	28.6	28.0	338702	6	US-10-087-192-292	Sequence 292, App
	39	28.4	27.8	649	12	US-10-301-480-387907	Sequence 387907,
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	43	28.4	27.8	1482	3	US-09-828-523A-21	Sequence 21, Appl
	44	28.4	27.8	1482	3	US-09-966-521-17	Sequence 17, Appl
	45	28.4	27.8	1482	7	US-10-429-094-17	Sequence 17, Appl
	46	28.4	27.8	1509	3	US-09-828-523A-89	Sequence 89, Appl
	47	28.4	27.8	1509	3	US-09-966-521-83	Sequence 83, Appl
	48	28.4	27.8	1509	7	US-10-429-094-83	Sequence 83, Appl
c	49	28.4	27.8	1598	9	US-10-739-930-219	Sequence 219, App
c	50	28.4	27.8	493999	9	US-10-719-993-6787	Sequence 6787, Ap
	51	28.4	27.8	1223197	6	US-10-027-632-179264	Sequence 179264,
	52	28.4	27.8	1223197	7	US-10-027-632-179264	Sequence 179264,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-4.rnpbn.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 536-4.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:39:12 ; Search time 105.904 Seconds
                                            (without alignments)
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      Pred. No. is the number of results predicted by chance to have a
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Result          Query
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3	27.6	27.1	2538	7	US-11-217-529-81150	Sequence 81150, A
c 4	27.4	26.9	808	7	US-11-266-748A-366887	Sequence 366887,
c 5	27.4	26.9	808	7	US-11-266-748A-388674	Sequence 388674,
6	27.4	26.9	808	7	US-11-266-748A-450266	Sequence 450266,
c 7	27.4	26.9	1184	7	US-11-266-748A-302007	Sequence 302007,
8	27.2	26.7	156655	7	US-11-266-748A-24308	Sequence 24308, A
9	26.8	26.3	2426	7	US-11-266-748A-188428	Sequence 188428,
c 10	26.8	26.3	2426	7	US-11-266-748A-242364	Sequence 242364,
11	26.8	26.3	66109	7	US-11-266-748A-32175	Sequence 32175, A
12	26.8	26.3	198285	7	US-11-266-748A-59857	Sequence 59857, A
13	26.6	26.1	2432	6	US-10-449-902-9730	Sequence 9730, Ap
c 14	26.6	26.1	160820	7	US-11-266-748A-22501	Sequence 22501, A
15	26.4	25.9	1000	7	US-11-266-748A-198483	Sequence 198483,
16	26.4	25.9	684973	7	US-11-266-748A-32013	Sequence 32013, A
c 17	26.2	25.7	1071650	7	US-11-266-748A-22664	Sequence 22664, A
18	26	25.5	1131	7	US-11-217-529-82398	Sequence 82398, A
19	26	25.5	2552	7	US-11-297-315-11	Sequence 11, Appl
20	26	25.5	2552	7	US-11-297-315-12	Sequence 12, Appl
c 21	26	25.5	128978	7	US-11-266-748A-61436	Sequence 61436, A
c 22	25.8	25.3	554	6	US-10-488-619-125	Sequence 125, App
23	25.8	25.3	1000	7	US-11-266-748A-115244	Sequence 115244,
c 24	25.8	25.3	1000	7	US-11-266-748A-157408	Sequence 157408,
c 25	25.8	25.3	1000	7	US-11-266-748A-202572	Sequence 202572,
26	25.8	25.3	1000	7	US-11-266-748A-392415	Sequence 392415,
27	25.8	25.3	1000	7	US-11-266-748A-393951	Sequence 393951,
c 28	25.8	25.3	1000	7	US-11-266-748A-464997	Sequence 464997,
c 29	25.8	25.3	1000	7	US-11-266-748A-483133	Sequence 483133,
30	25.8	25.3	1841	7	US-11-266-748A-20889	Sequence 20889, A
31	25.8	25.3	1854	7	US-11-266-748A-186789	Sequence 186789,
32	25.8	25.3	2237	6	US-10-449-902-27089	Sequence 27089, A
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34	25.6	25.1	1253	6	US-10-449-902-1062	Sequence 1062, Ap
35	25.6	25.1	1512	6	US-10-449-902-22374	Sequence 22374, A
36	25.6	25.1	4611	7	US-11-217-529-191207	Sequence 191207,
c 37	25.4	24.9	1453	7	US-11-216-545-1367	Sequence 1367, Ap
38	25.4	24.9	1237661	7	US-11-266-748A-29041	Sequence 29041, A
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c 42	25.2	24.7	597	7	US-11-266-748A-138479	Sequence 138479,
c 43	25.2	24.7	814	7	US-11-266-748A-44067	Sequence 44067, A
c 44	25.2	24.7	815	7	US-11-266-748A-177083	Sequence 177083,
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c 53	25.2	24.7	1114	7	US-11-266-748A-277130	Sequence 277130,
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c 55	25.2	24.7	1233	7	US-11-266-748A-249171	Sequence 249171,
c 56	25.2	24.7	1235	7	US-11-266-748A-188440	Sequence 188440,
c 57	25.2	24.7	1282	7	US-11-266-748A-25905	Sequence 25905, A
c 58	25.2	24.7	1471	7	US-11-266-748A-3809	Sequence 3809, Ap
c 59	25.2	24.7	3486	6	US-10-517-441-556	Sequence 556, App

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-4.rst.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-4.rst.

start

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                     GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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                                          1541.534 Million cell updates/sec

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                 9:  gb_est8:*
                 10:  gb_est9:*
                 11:  gb_gss1:*
                 12:  gb_gss2:*
                 13:  gb_gss3:*
                 14:  gb_gss4:*

         Pred. No. is the number of results predicted by chance to have a
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34.4	33.7	858	12	CC516020	CC516020 CH240_361
	2	32.6	32.0	781	10	DV571328	DV571328 0058P0009
	3	32.4	31.8	352	1	AA483240	AA483240 ne87h09.s
c	4	32.2	31.6	420	11	AQ132470	AQ132470 HS_3003_A
c	5	32	31.4	358	4	BX117527	BX117527 BX117527
c	6	31.8	31.2	741	11	BH920547	BH920547 odh72g09.
c	7	31.6	31.0	583	12	CE765576	CE765576 tigr-gss-
c	8	31.6	31.0	730	3	BU007004	BU007004 QGH13A24.
	9	31.6	31.0	885	10	DV000824	DV000824 CNB209-D0
	10	31.6	31.0	963	10	DW031234	DW031234 CFW210-C0
	11	31.6	31.0	1070	10	DW671063	DW671063 CNB363-C1
	12	31.6	31.0	1077	9	DN715926	DN715926 CNB11-H12
	13	31.6	31.0	1138	10	DW664718	DW664718 CNB327-C0
	14	31.6	31.0	1211	9	DN713155	DN713155 CNB06-D06
	15	31.6	31.0	1393	9	DN687169	DN687169 CGX51-C11
c	16	31.4	30.8	417	4	BY266232	BY266232 BY266232
	17	31.4	30.8	487	3	BQ488932	BQ488932 30-E9135-
	18	31.4	30.8	572	11	AQ771527	AQ771527 HS_5399_A
c	19	31.4	30.8	659	12	CE683008	CE683008 tigr-gss-
	20	31.4	30.8	850	8	CV301701	CV301701 MM12_H02
c	21	31.2	30.6	203	1	AV264282	AV264282 AV264282
	22	31.2	30.6	710	11	AZ261111	AZ261111 RPCI-23-1
	23	31.2	30.6	766	10	DR814197	DR814197 ZM_BFb004
	24	31.2	30.6	788	14	DU654335	DU654335 OG_ABa005
	25	31.2	30.6	791	2	BG501875	BG501875 602548974
	26	31.2	30.6	798	9	DB293067	DB293067 DB293067
c	27	31.2	30.6	873	14	CR180171	CR180171 Forward s
c	28	31.2	30.6	1133	14	AG604607	AG604607 Mus muscu
c	29	30.8	30.2	593	5	CK876164	CK876164 SGP137428
c	30	30.8	30.2	745	3	BQ853453	BQ853453 QGB20I21.
c	31	30.8	30.2	860	12	CL098155	CL098155 ISB1-30O7
	32	30.8	30.2	867	1	AJ821715	AJ821715 AJ821715
c	33	30.8	30.2	877	10	DT749554	DT749554 EST118340
c	34	30.6	30.0	513	9	DN777882	DN777882 E5778 [C2
	35	30.6	30.0	634	3	BW273512	BW273512 BW273512
	36	30.6	30.0	644	5	CK534132	CK534132 rswgb0_00
c	37	30.6	30.0	702	3	BQ510748	BQ510748 EST618163
	38	30.6	30.0	722	14	AG162641	AG162641 Pan trogl
c	39	30.4	29.8	198	14	BX964864	BX964864 Forward s
	40	30.2	29.6	344	7	AW860820	AW860820 QV0-CT038
	41	30.2	29.6	669	14	AG048006	AG048006 Pan trogl
	42	30.2	29.6	730	10	DT561959	DT561959 EST107259
c	43	30	29.4	515	13	CZ552456	CZ552456 M0002497
	44	30	29.4	720	11	BH932160	BH932160 odh58g08.
c	45	30	29.4	834	13	CW704484	CW704484 AIAA-aaa8
c	46	30	29.4	1097	1	AL534616	AL534616 AL534616
	47	30	29.4	1497	2	BF788820	BF788820 602110529
c	48	29.8	29.2	384	13	CL887940	CL887940 abf87c05.
c	49	29.8	29.2	540	4	CB396886	CB396886 OSTR180H4
c	50	29.8	29.2	643	14	CR076760	CR076760 Forward s
c	51	29.8	29.2	659	11	AZ226184	AZ226184 RPCI-23-9
	52	29.8	29.2	661	4	CA118151	CA118151 SCBGLR108
	53	29.8	29.2	663	12	CC154488	CC154488 CSU-K34.1

SCORE Search Results Details for Application 1C 630-536-5.rge

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:

```
                          GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 03:55:42 ; Search time 357.646 Seconds
                                           (without alignments)
                                           4291.222 Million cell updates/sec

Title:           US-10-630-536-5
Perfect score:   24
Sequence:        1 atttgtcggaaggtcgcagtgaga 24

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	24	2	CS001824	CS001824 Sequence
2	24	100.0	147	2	CS001827	CS001827 Sequence
3	24	100.0	96210	15	YPPMT1	AL117211 Yersinia
4	24	100.0	100984	15	AF053947	AF053947 Yersinia
c 5	24	100.0	100990	2	AR487637	AR487637 Sequence
c 6	24	100.0	100990	15	AF074611	AF074611 Yersinia
7	24	100.0	106516	15	STYPPHCM2	AL513384 Salmonell
8	24	100.0	106642	15	AE017045	AE017045 Yersinia
9	24	100.0	137036	15	AJ698720	AJ698720 Yersinia
c 10	19.2	80.0	198282	12	CT025723	CT025723 Drosophil
c 11	18.2	75.8	1014	6	AY336501	AY336501 Mus muscu
12	18.2	75.8	1954	6	BC043679	BC043679 Mus muscu
c 13	18.2	75.8	2446	13	AY095069	AY095069 Drosophil
c 14	18.2	75.8	3461	2	CQ578330	CQ578330 Sequence
15	18.2	75.8	3502	6	MUSGTPAAP	D11374 Mus musculu
16	18.2	75.8	3519	2	AR052339	AR052339 Sequence
17	18.2	75.8	3519	2	AR093112	AR093112 Sequence
18	18.2	75.8	3519	2	E11890	E11890 cDNA encodi
19	18.2	75.8	3519	2	AR214171	AR214171 Sequence
20	18.2	75.8	3569	6	BC054824	BC054824 Mus muscu
21	18.2	75.8	3741	6	AK220472	AK220472 Mus muscu
22	18.2	75.8	6645	2	AR052341	AR052341 Sequence
23	18.2	75.8	6645	2	AR093114	AR093114 Sequence
24	18.2	75.8	6645	2	E11892	E11892 DNA encodin
25	18.2	75.8	6645	2	AR214173	AR214173 Sequence
26	18.2	75.8	12432	6	D87849	D87849 Mus musculu
c 27	18.2	75.8	34159	13	DMC165H7	AL009188 Drosophil
c 28	18.2	75.8	38591	13	CEC54E10	Z81487 Caenorhabdi
c 29	18.2	75.8	42473	12	AC020093	AC020093 Drosophil
30	18.2	75.8	50531	5	AC145467	AC145467 Pan trogl
c 31	18.2	75.8	87740	13	AE003417_3	Continuation (4 of
c 32	18.2	75.8	117049	5	AC018987	AC018987 Homo sapi
c 33	18.2	75.8	118572	5	AL133408	AL133408 Human DNA
34	18.2	75.8	163878	6	AC134563	AC134563 Mus muscu
c 35	18.2	75.8	168639	5	AC021818	AC021818 Homo sapi
c 36	18.2	75.8	170186	13	AC105774	AC105774 Drosophil
37	18.2	75.8	170795	12	AC021346	AC021346 Homo sapi
38	18.2	75.8	171990	6	AC117240	AC117240 Mus muscu
39	18.2	75.8	174752	5	AC146075	AC146075 Pan trogl
40	18.2	75.8	192074	6	AL840639	AL840639 Mouse DNA
c 41	18.2	75.8	200896	6	AC159251	AC159251 Mus muscu
42	18.2	75.8	243976	6	AC159193	AC159193 Mus muscu
c 43	17.8	74.2	4843	5	AB035196	AB035196 Homo sapi
44	17.8	74.2	6154	15	AF337952	AF337952 Azoarcus
45	17.8	74.2	7037	2	AX344372	AX344372 Sequence
c 46	17.8	74.2	105321	5	AL928711	AL928711 Human DNA
47	17.8	74.2	110000	12	CT005250_0	CT005250 Leishmani
c 48	17.8	74.2	110000	15	CR555306_13	Continuation (14 o
49	17.8	74.2	110000	15	AE017143_08	Continuation (9 of
50	17.8	74.2	124581	5	BX649364	BX649364 Human DNA
51	17.8	74.2	136088	5	AL139426	AL139426 Human DNA
c 52	17.8	74.2	173910	5	BX855602	BX855602 Human DNA
c 53	17.8	74.2	186829	5	BX640519	BX640519 Human DNA
54	17.6	73.3	633	7	BV279472	BV279472 S232P6452
55	17.6	73.3	667	7	BV638707	BV638707 S216P6176
56	17.6	73.3	2656	13	AF541879	AF541879 Branchios

SCORE Search Results Details for Application 10(
Search Result us-10-630-536-5.rng.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:

```
                       GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 03:53:57 ; Search time 144.689 Seconds
                                          (without alignments)
                                          1156.508 Million cell updates/sec

Title:          US-10-630-536-5
Perfect score:  24
Sequence:       1 atttgtcggaaggtcgcagtgaga 24

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      N_Geneseq_8:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	14	ADV04870	Adv04870 Yersinia
	2	24	100.0	147	14	ADV04873	Adv04873 Yersinia
c	3	24	100.0	100990	12	ADJ94407	Adj94407 Yersinia
c	4	18.2	75.8	3461	4	ABL05898	Abl05898 Drosophil
	5	18.2	75.8	3500	2	AAT72782	Aat72782 Mouse int
	6	18.2	75.8	3519	2	AAT65000	Aat65000 Mouse cel
	7	18.2	75.8	6645	2	AAT65002	Aat65002 Mouse cel
	8	17.8	74.2	7037	6	ABK31376	Abk31376 Signal tr
c	9	17.6	73.3	10497	4	AAK67302	Aak67302 Human imm
	10	17.6	73.3	10497	4	AAK83166	Aak83166 Human imm
	11	17.6	73.3	171324	11	ACN43892	Acn43892 Mouse gen
	12	17.2	71.7	19639	2	AAX23524	Aax23524 O. longis
	13	17.2	71.7	76574	4	ABL03438	Abl03438 Drosophil
c	14	17.2	71.7	226215	11	ACN45146	Acn45146 Human gen
	15	16.8	70.0	364	5	AAF65355	Aaf65355 Novel hum
c	16	16.8	70.0	4296	4	ABL02046	Abl02046 Drosophil
c	17	16.8	70.0	4801	4	ABL26362	Abl26362 Drosophil
c	18	16.6	69.2	65	6	ABN53376	Abn53376 Mouse spl
c	19	16.6	69.2	100	8	ACD77600	Acd77600 E. coli K
c	20	16.6	69.2	100	8	ACD77601	Acd77601 E. coli K
	21	16.6	69.2	387	10	ACF69316	Acf69316 Photorhab
c	22	16.6	69.2	402	4	AAH84583	Aah84583 E. coli g
c	23	16.6	69.2	545	12	ADL88187	Adl88187 DNA up-re
c	24	16.6	69.2	545	12	ADL88186	Adl88186 DNA up-re
	25	16.6	69.2	834	12	ADO35971	Ado35971 Novel mou
	26	16.6	69.2	906	4	AAK83226	Aak83226 Human imm
c	27	16.6	69.2	998	6	ABT07198	Abt07198 Human CpG
	28	16.6	69.2	1167	13	ADX12937	Adx12937 Plant ful
	29	16.6	69.2	1280	12	ADI82283	Adi82283 Human DNA
	30	16.6	69.2	1720	2	AAQ78916	Aaq78916 Non-typab
	31	16.6	69.2	3599	11	ACN91978	Acn91978 Breast ca
	32	16.6	69.2	3864	13	ADS96669	Ads96669 Drosophil
	33	16.6	69.2	3907	14	ADY17893	Ady17893 DNA encod
	34	16.6	69.2	4003	4	ABL09841	Abl09841 Drosophil
c	35	16.6	69.2	4151	2	AAZ23663	Aaz23663 B. bassia
	36	16.6	69.2	4289	13	ADR07156	Adr07156 Full leng
	37	16.6	69.2	6237	6	ABL32359	Abl32359 Human imm
	38	16.6	69.2	6286	4	AAK83148	Aak83148 Human imm
	39	16.6	69.2	6751	4	AAK83163	Aak83163 Human imm
	40	16.6	69.2	6767	4	AAK83147	Aak83147 Human imm
	41	16.6	69.2	6943	4	AAK83198	Aak83198 Human imm
c	42	16.6	69.2	7004	13	ADT05477	Adt05477 Haemophil
c	43	16.6	69.2	7038	4	ABL09840	Abl09840 Drosophil
	44	16.6	69.2	7633	4	AAK83159	Aak83159 Human imm
	45	16.6	69.2	7906	4	AAK83154	Aak83154 Human imm
	46	16.6	69.2	9133	4	AAK83165	Aak83165 Human imm
	47	16.6	69.2	9217	4	AAK83151	Aak83151 Human imm
c	48	16.6	69.2	9439	4	AAK67312	Aak67312 Human imm
	49	16.6	69.2	9439	4	AAK83168	Aak83168 Human imm
	50	16.6	69.2	9832	4	AAK83150	Aak83150 Human imm
	51	16.6	69.2	11428	4	AAK83156	Aak83156 Human imm
	52	16.6	69.2	11744	4	AAK83160	Aak83160 Human imm
c	53	16.6	69.2	11853	4	AAK67297	Aak67297 Human imm
	54	16.6	69.2	11853	4	AAK83162	Aak83162 Human imm
	55	16.6	69.2	14258	4	AAK83210	Aak83210 Human imm
	56	16.6	69.2	14260	4	AAK83183	Aak83183 Human imm

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-5.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 5.rni.

start

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                        GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 04:28:37 ; Search time 29.4545 Seconds
                                          (without alignments)
                                          1524.607 Million cell updates/sec

Title:          US-10-630-536-5
Perfect score:  24
Sequence:       1 atttgtcggaaggtcgcagtgaga 24

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:     2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      Issued_Patents_NA:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                         %
Result              Query
   No.    Score  Match Length DB   ID                        Description
```

c	1	24	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
	2	18.2	75.8	3519	2	US-08-380-403A-1	Sequence 1, Appli
	3	18.2	75.8	3519	2	US-08-895-628-1	Sequence 1, Appli
	4	18.2	75.8	3519	3	US-08-895-810D-1	Sequence 1, Appli
	5	18.2	75.8	6645	2	US-08-380-403A-4	Sequence 4, Appli
	6	18.2	75.8	6645	2	US-08-895-628-4	Sequence 4, Appli
	7	18.2	75.8	6645	3	US-08-895-810D-4	Sequence 4, Appli
c	8	16.6	69.2	402	3	US-09-711-164-211	Sequence 211, App
c	9	16.6	69.2	601	3	US-09-949-016-87151	Sequence 87151, A
c	10	16.6	69.2	601	3	US-09-949-016-109809	Sequence 109809,
	11	16.6	69.2	601	3	US-09-949-016-152778	Sequence 152778,
	12	16.6	69.2	601	3	US-09-949-016-152779	Sequence 152779,
c	13	16.6	69.2	998	3	US-09-775-398-15	Sequence 15, Appl
	14	16.6	69.2	1720	2	US-08-457-997B-1	Sequence 1, Appli
	15	16.6	69.2	1720	3	US-08-467-722A-1	Sequence 1, Appli
	16	16.6	69.2	1720	3	US-09-451-184-1	Sequence 1, Appli
c	17	16.6	69.2	7649	3	US-09-949-016-16033	Sequence 16033, A
c	18	16.6	69.2	72049	3	US-09-544-398B-9	Sequence 9, Appli
c	19	16.6	69.2	72049	3	US-09-543-771B-9	Sequence 9, Appli
	20	16.6	69.2	92681	3	US-09-949-016-14772	Sequence 14772, A
c	21	16.6	69.2	140844	3	US-09-949-016-14199	Sequence 14199, A
	22	16.2	67.5	576	3	US-09-252-991A-4866	Sequence 4866, Ap
	23	16.2	67.5	768	3	US-09-252-991A-12489	Sequence 12489, A
	24	16.2	67.5	1069	3	US-09-270-767-11416	Sequence 11416, A
	25	16.2	67.5	1230	3	US-09-134-000C-2763	Sequence 2763, Ap
c	26	16.2	67.5	1260	3	US-09-252-991A-4852	Sequence 4852, Ap
c	27	16.2	67.5	2492	3	US-09-973-278-708	Sequence 708, App
	28	16.2	67.5	153866	3	US-09-949-016-16919	Sequence 16919, A
c	29	16	66.7	700	3	US-09-735-271-761	Sequence 761, App
c	30	16	66.7	1075	3	US-09-270-767-28307	Sequence 28307, A
c	31	16	66.7	1324	3	US-09-270-767-12525	Sequence 12525, A
	32	16	66.7	54550	3	US-10-327-189-42	Sequence 42, Appl
c	33	16	66.7	276687	3	US-09-949-016-13840	Sequence 13840, A
	34	15.8	65.8	206	3	US-09-513-999C-28375	Sequence 28375, A
	35	15.8	65.8	601	3	US-09-949-016-53929	Sequence 53929, A
	36	15.8	65.8	601	3	US-09-949-016-53930	Sequence 53930, A
	37	15.8	65.8	601	3	US-09-949-016-53931	Sequence 53931, A
c	38	15.8	65.8	601	3	US-09-949-001-227	Sequence 227, App
c	39	15.8	65.8	601	3	US-09-949-001-501	Sequence 501, App
	40	15.8	65.8	601	3	US-09-949-002-2320	Sequence 2320, Ap
	41	15.8	65.8	601	3	US-09-949-002-4920	Sequence 4920, Ap
	42	15.8	65.8	1172	3	US-09-902-540-6171	Sequence 6171, Ap
c	43	15.8	65.8	1621	3	US-09-902-540-309	Sequence 309, App
	44	15.8	65.8	2139	3	US-09-949-002-142	Sequence 142, App
	45	15.8	65.8	4173	3	US-09-949-002-61	Sequence 61, Appl
c	46	15.8	65.8	36148	3	US-09-949-016-12969	Sequence 12969, A
	47	15.8	65.8	70313	3	US-09-949-002-714	Sequence 714, App
	48	15.8	65.8	72347	3	US-09-949-002-633	Sequence 633, App
	49	15.8	65.8	75176	3	US-09-949-016-13300	Sequence 13300, A
c	50	15.8	65.8	192302	3	US-09-949-016-15270	Sequence 15270, A
c	51	15.8	65.8	246230	3	US-09-949-016-17019	Sequence 17019, A
c	52	15.8	65.8	246230	3	US-09-949-016-17020	Sequence 17020, A
c	53	15.8	65.8	246230	3	US-09-949-016-17021	Sequence 17021, A
c	54	15.8	65.8	246230	3	US-09-949-016-17022	Sequence 17022, A
c	55	15.8	65.8	312957	3	US-09-949-001-31	Sequence 31, Appl
c	56	15.8	65.8	312972	3	US-09-949-001-34	Sequence 34, Appl
c	57	15.8	65.8	325791	3	US-09-768-185A-1	Sequence 1, Appli
c	58	15.6	65.0	144	3	US-09-513-999C-29481	Sequence 29481, A
	59	15.6	65.0	424	3	US-09-513-999C-9813	Sequence 9813, Ap
c	60	15.6	65.0	460	2	US-08-967-101-48	Sequence 48, Appl

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-5.rnpbm.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 536-5.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:38:10 ; Search time 334.105 Seconds
                                           (without alignments)
                                           882.666 Million cell updates/sec

Title:           US-10-630-536-5
Perfect score:   24
Sequence:        1 atttgtcggaaggtcgcagtgaga 24

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       Published_Applications_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	24	100.0	147	11	US-10-630-536-8	Sequence 8, Appli
	3	18.8	78.3	600	10	US-10-972-079-79803	Sequence 79803, A
c	4	18.2	75.8	3461	13	US-11-097-143-6088	Sequence 6088, Ap
c	5	17.6	73.3	201	9	US-10-741-600-59349	Sequence 59349, A
	6	17.6	73.3	581	4	US-09-925-065A-636311	Sequence 636311,
	7	17.6	73.3	581	4	US-09-925-065A-636312	Sequence 636312,
	8	17.6	73.3	581	5	US-09-925-065A-636311	Sequence 636311,
	9	17.6	73.3	581	5	US-09-925-065A-636312	Sequence 636312,
c	10	17.6	73.3	818	6	US-10-027-632-325318	Sequence 325318,
c	11	17.6	73.3	818	7	US-10-027-632-325318	Sequence 325318,
	12	17.6	73.3	171324	6	US-10-087-192-67	Sequence 67, Appl
c	13	17.6	73.3	385320	9	US-10-741-600-17796	Sequence 17796, A
c	14	17.6	73.3	1080000	10	US-10-928-446A-1	Sequence 1, Appli
c	15	17.6	73.3	1080000	10	US-10-928-446A-181	Sequence 181, App
c	16	17.6	73.3	1080000	10	US-10-928-446A-183	Sequence 183, App
c	17	17.6	73.3	1080000	10	US-10-928-446A-185	Sequence 185, App
c	18	17.6	73.3	1080000	10	US-10-928-446A-187	Sequence 187, App
c	19	17.6	73.3	1080000	10	US-10-928-446A-189	Sequence 189, App
c	20	17.6	73.3	1080000	10	US-10-928-446A-191	Sequence 191, App
c	21	17.6	73.3	1080000	10	US-10-928-446A-193	Sequence 193, App
c	22	17.6	73.3	1080000	10	US-10-928-446A-195	Sequence 195, App
c	23	17.6	73.3	1080000	10	US-10-928-446A-197	Sequence 197, App
c	24	17.6	73.3	1080000	10	US-10-928-446A-199	Sequence 199, App
c	25	17.6	73.3	1080000	10	US-10-928-446A-201	Sequence 201, App
c	26	17.4	72.5	25	9	US-10-719-900-404868	Sequence 404868,
c	27	17.2	71.7	25	9	US-10-719-900-134888	Sequence 134888,
c	28	17.2	71.7	427	4	US-09-925-065A-839028	Sequence 839028,
c	29	17.2	71.7	427	5	US-09-925-065A-839028	Sequence 839028,
	30	17.2	71.7	472	4	US-09-925-065A-269771	Sequence 269771,
	31	17.2	71.7	472	4	US-09-925-065A-269772	Sequence 269772,
	32	17.2	71.7	472	4	US-09-925-065A-269773	Sequence 269773,
	33	17.2	71.7	472	5	US-09-925-065A-269771	Sequence 269771,
	34	17.2	71.7	472	5	US-09-925-065A-269772	Sequence 269772,
	35	17.2	71.7	472	5	US-09-925-065A-269773	Sequence 269773,
	36	17.2	71.7	479	12	US-10-301-480-347316	Sequence 347316,
	37	17.2	71.7	479	12	US-10-301-480-347317	Sequence 347317,
	38	17.2	71.7	479	12	US-10-301-480-347318	Sequence 347318,
	39	17.2	71.7	479	12	US-10-301-480-960725	Sequence 960725,
	40	17.2	71.7	479	12	US-10-301-480-960726	Sequence 960726,
	41	17.2	71.7	479	12	US-10-301-480-960727	Sequence 960727,
c	42	17.2	71.7	529	4	US-09-925-065A-325085	Sequence 325085,
c	43	17.2	71.7	529	5	US-09-925-065A-325085	Sequence 325085,
c	44	17.2	71.7	593	4	US-09-925-065A-570380	Sequence 570380,
c	45	17.2	71.7	593	4	US-09-925-065A-570381	Sequence 570381,
c	46	17.2	71.7	593	5	US-09-925-065A-570380	Sequence 570380,
c	47	17.2	71.7	593	5	US-09-925-065A-570381	Sequence 570381,
	48	17.2	71.7	606	12	US-10-301-480-53323	Sequence 53323, A
	49	17.2	71.7	606	12	US-10-301-480-666732	Sequence 666732,
	50	17.2	71.7	619	6	US-10-027-632-253142	Sequence 253142,
	51	17.2	71.7	619	7	US-10-027-632-253142	Sequence 253142,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-5.rn

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 5.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 04:39:12 ; Search time 24.9187 Seconds
                                          (without alignments)
                                          1138.902 Million cell updates/sec

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Sequence:       1 atttgtcggaaggtcgcagtgaga 24

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters:      1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Database :      Published_Applications_NA_New:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result              Query
   No.    Score  Match  Length  DB  ID                           Description
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     1    17.2   71.7    1870    6  US-10-449-902-8774            Sequence 8774, Ap
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c	2	16.8	70.0	1382	7	US-11-266-748A-167039	Sequence 167039,
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c	4	16.8	70.0	1839	7	US-11-266-748A-259273	Sequence 259273,
	5	16.8	70.0	1839	7	US-11-266-748A-319790	Sequence 319790,
	6	16.6	69.2	496	7	US-11-266-748A-95692	Sequence 95692, A
	7	16.6	69.2	496	7	US-11-266-748A-113285	Sequence 113285,
c	8	16.6	69.2	496	7	US-11-266-748A-148503	Sequence 148503,
	9	16.6	69.2	822	7	US-11-266-748A-273220	Sequence 273220,
c	10	16.6	69.2	822	7	US-11-266-748A-333737	Sequence 333737,
	11	16.6	69.2	1505	6	US-10-449-902-4636	Sequence 4636, Ap
	12	16.6	69.2	1671	7	US-11-216-545-1388	Sequence 1388, Ap
c	13	16.6	69.2	1798	6	US-10-953-349-21708	Sequence 21708, A
	14	16.6	69.2	2091	6	US-10-449-902-20807	Sequence 20807, A
c	15	16.6	69.2	124048	7	US-11-266-748A-59707	Sequence 59707, A
c	16	16.6	69.2	156641	7	US-11-266-748A-61706	Sequence 61706, A
c	17	16.2	67.5	400	7	US-11-266-748A-219541	Sequence 219541,
	18	16.2	67.5	714	7	US-11-266-748A-418375	Sequence 418375,
	19	16	66.7	462	7	US-11-266-748A-270178	Sequence 270178,
c	20	16	66.7	462	7	US-11-266-748A-330695	Sequence 330695,
	21	16	66.7	638	7	US-11-266-748A-51873	Sequence 51873, A
c	22	16	66.7	1000	7	US-11-266-748A-204106	Sequence 204106,
	23	16	66.7	1233	7	US-11-266-748A-71926	Sequence 71926, A
	24	16	66.7	1233	7	US-11-266-748A-106932	Sequence 106932,
c	25	16	66.7	1233	7	US-11-266-748A-124737	Sequence 124737,
	26	16	66.7	1834	7	US-11-293-697-2209	Sequence 2209, Ap
	27	16	66.7	2391	7	US-11-217-529-2137	Sequence 2137, Ap
	28	16	66.7	2818	6	US-10-449-902-14998	Sequence 14998, A
	29	16	66.7	54550	7	US-11-318-813-42	Sequence 42, Appl
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	31	15.8	65.8	477	7	US-11-217-529-3681	Sequence 3681, Ap
c	32	15.8	65.8	872	7	US-11-266-748A-356713	Sequence 356713,
c	33	15.8	65.8	872	7	US-11-266-748A-386049	Sequence 386049,
	34	15.8	65.8	872	7	US-11-266-748A-440092	Sequence 440092,
	35	15.8	65.8	888	7	US-11-266-748A-49215	Sequence 49215, A
	36	15.8	65.8	888	7	US-11-266-748A-215068	Sequence 215068,
c	37	15.8	65.8	1000	7	US-11-266-748A-295338	Sequence 295338,
	38	15.8	65.8	1000	7	US-11-266-748A-346767	Sequence 346767,
c	39	15.8	65.8	1000	7	US-11-266-748A-408092	Sequence 408092,
	40	15.8	65.8	1000	7	US-11-266-748A-479138	Sequence 479138,
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	42	15.8	65.8	1344	7	US-11-266-748A-191166	Sequence 191166,
c	43	15.8	65.8	1344	7	US-11-266-748A-240222	Sequence 240222,
	44	15.8	65.8	1875	6	US-10-953-349-23838	Sequence 23838, A
	45	15.8	65.8	4345	7	US-11-266-748A-27300	Sequence 27300, A
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c	47	15.6	65.0	396	7	US-11-266-748A-428564	Sequence 428564,
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c	59	15.6	65.0	1000	7	US-11-266-748A-392248	Sequence 392248,
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	62	15.6	65.0	1000	7	US-11-266-748A-482966	Sequence 482966,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-5.rst.

<u>Score Home Page</u>   <u>Retrieve Application List</u>   <u>SCORE System Overview</u>   <u>SCORE FAQ</u>   <u>Comments / Suggestions</u>

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-5.rst.

<u>start</u>

<u>Go Back to previous page</u>

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:17:07 ; Search time 870.603 Seconds
                                           (without alignments)
                                           1541.534 Million cell updates/sec

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Perfect score:   24
Sequence:        1 atttgtcggaaggtcgcagtgaga 24

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       EST:*
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                 12:  gb_gss2:*
                 13:  gb_gss3:*
                 14:  gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	4	18.2	75.8	250	10	W43945	W43945 mc72c01.r1
	5	18.2	75.8	431	1	AA646761	AA646761 ve43c10.r
	6	18.2	75.8	439	2	BG145962	BG145962 uu95a07.y
	7	18.2	75.8	468	10	W83596	W83596 mf30c03.r1
	8	18.2	75.8	499	1	AI182978	AI182978 ub92a11.r
	9	18.2	75.8	546	1	AI182158	AI182158 uc64b11.r
	10	18.2	75.8	548	1	AA475649	AA475649 vh22e04.r
c	11	18.2	75.8	549	3	BU670475	BU670475 MC01058F0
	12	18.2	75.8	569	1	AA272920	AA272920 va41f02.r
	13	18.2	75.8	573	1	AA273284	AA273284 vc01c04.r
	14	18.2	75.8	588	2	BG228327	BG228327 ux41f08.x
	15	18.2	75.8	596	5	CK133093	CK133093 RE15472.3
	16	18.2	75.8	644	10	W57213	W57213 md59e09.r1
	17	18.2	75.8	646	1	AI154692	AI154692 ud37f07.r
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	19	18.2	75.8	649	7	AW476530	AW476530 uq77c12.y
	20	18.2	75.8	668	2	BI082542	BI082542 602877919
	21	18.2	75.8	686	1	AV088479	AV088479 AV088479
c	22	18.2	75.8	829	13	DU091573	DU091573 100803 To
	23	18.2	75.8	843	2	BG975564	BG975564 602845268
	24	18.2	75.8	856	4	CA977500	CA977500 AGENCOURT
	25	18.2	75.8	998	7	BF124739	BF124739 601761422
	26	18.2	75.8	999	14	CNS06ZW6	AL422860 T3 end of
c	27	18.2	75.8	1160	6	AK005865	AK005865 Mus muscu
	28	18.2	75.8	2802	6	AK028151	AK028151 Mus muscu
	29	18.2	75.8	3457	6	AK169945	AK169945 Mus muscu
	30	18.2	75.8	3520	6	AK149669	AK149669 Mus muscu
	31	18.2	75.8	3538	6	AK137578	AK137578 Mus muscu
	32	18.2	75.8	3813	6	AK156280	AK156280 Mus muscu
c	33	17.8	74.2	655	11	BZ116006	BZ116006 CH230-510
	34	17.8	74.2	659	11	BH887754	BH887754 LB01648a.
c	35	17.8	74.2	667	7	BB095304	BB095304 BB095304
c	36	17.8	74.2	747	8	CN039648	CN039648 nm_32h_o2
c	37	17.8	74.2	800	2	BG195843	BG195843 RST15104
c	38	17.8	74.2	810	13	DU119015	DU119015 KBrH097P1
c	39	17.8	74.2	812	10	DT829517	DT829517 LB0044.CR
c	40	17.8	74.2	822	10	DT857579	DT857579 LB00532.C
c	41	17.8	74.2	949	5	CK404641	CK404641 AUF_IfHdk
c	42	17.8	74.2	1394	12	CC258210	CC258210 CH261-175
c	43	17.6	73.3	262	14	CR089939	CR089939 Reverse s
	44	17.6	73.3	294	8	CV427205	CV427205 RC6-ET008
c	45	17.6	73.3	406	8	CO593747	CO593747 DG2-86c13
c	46	17.6	73.3	427	12	CE438745	CE438745 tigr-gss-
	47	17.6	73.3	453	3	BU830938	BU830938 T015A11 P
c	48	17.6	73.3	513	8	CO616233	CO616233 DG9-155a1
	49	17.6	73.3	522	2	BF963391	BF963391 QV2-NN004
c	50	17.6	73.3	542	8	CO688501	CO688501 DG11-246o
	51	17.6	73.3	548	11	AQ484393	AQ484393 RPCI-11-2
	52	17.6	73.3	585	1	AL683669	AL683669 AL683669
c	53	17.6	73.3	609	2	BG348685	BG348685 dad16d09.

SCORE Search Results Details for Application 1C 630-536-6.rge

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
start | next page

```
                     GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        July  1, 2006, 03:55:42 ; Search time 342.744 Seconds
                                         (without alignments)
                                         4291.222 Million cell updates/sec

Title:         US-10-630-536-6
Perfect score: 23
Sequence:      1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :     GenEmbl:*
               1:  gb_env:*
               2:  gb_pat:*
               3:  gb_ph:*
               4:  gb_pl:*
               5:  gb_pr:*
               6:  gb_ro:*
               7:  gb_sts:*
               8:  gb_sy:*
               9:  gb_un:*
               10:  gb_vi:*
               11:  gb_ov:*
               12:  gb_htg:*
               13:  gb_in:*
               14:  gb_om:*
               15:  gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     -score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23	100.0	23	2	CS001825	CS001825 Sequence
c	2	23	100.0	147	2	CS001827	CS001827 Sequence
c	3	23	100.0	96210	15	YPPMT1	AL117211 Yersinia
c	4	23	100.0	100984	15	AF053947	AF053947 Yersinia
	5	23	100.0	100990	2	AR487637	AR487637 Sequence
	6	23	100.0	100990	15	AF074611	AF074611 Yersinia
c	7	23	100.0	106516	15	STYPPHCM2	AL513384 Salmonell
c	8	23	100.0	106642	15	AE017045	AE017045 Yersinia
c	9	23	100.0	137036	15	AJ698720	AJ698720 Yersinia
	10	19.8	86.1	110000	4	AP008216_068	Continuation (69 o
	11	19.8	86.1	110000	4	AE016959_068	Continuation (69 o
	12	19.8	86.1	137568	4	AC093178	AC093178 Oryza sat
c	13	19.4	84.3	12026	15	AE005109	AE005109 Halobacte
	14	19.4	84.3	189230	12	AC120836	AC120836 Mus muscu
	15	19.4	84.3	209356	6	AL806525	AL806525 Mouse DNA
c	16	18.4	80.0	103975	4	AY702979	AY702979 Capsicum
	17	18.2	79.1	110000	4	AP008212_114	Continuation (115
	18	18.2	79.1	110000	4	AP008207_032	Continuation (33 o
	19	18.2	79.1	133019	4	AP006054	AP006054 Oryza sat
	20	18.2	79.1	167761	4	AP003209	AP003209 Oryza sat
c	21	17.8	77.4	8524	15	AB100500	AB100500 Selenomon
	22	17.8	77.4	44117	13	AY190946	AY190946 Drosophil
	23	17.8	77.4	110000	4	CR382131_13	Continuation (14 o
c	24	17.8	77.4	110000	12	CT005271_16	Continuation (17 o
c	25	17.8	77.4	110000	15	AE004969_06	Continuation (7 of
	26	17.8	77.4	110000	15	CP000100_08	Continuation (9 of
c	27	17.8	77.4	110000	15	AP008231_07	Continuation (8 of
c	28	17.4	75.7	1432	4	AK107315	AK107315 Oryza sat
	29	17.4	75.7	110000	15	BA000040_53	Continuation (54 o
	30	17.2	74.8	738	2	AX436604	AX436604 Sequence
c	31	17.2	74.8	9680	15	AY972822	AY972822 Rhodother
c	32	17.2	74.8	56390	2	CQ603410	CQ603410 Sequence
c	33	17.2	74.8	64799	13	CP000212	CP000212 Drosophil
c	34	17.2	74.8	66833	12	AC101655	AC101655 Mus muscu
	35	17.2	74.8	110000	4	AP008213_076	Continuation (77 o
	36	17.2	74.8	110000	4	AP008218_245	Continuation (246
	37	17.2	74.8	110000	12	AP006491_0	AP006491 Cyanidios
	38	17.2	74.8	110000	15	AE002098_14	Continuation (15 o
c	39	17.2	74.8	110000	15	AE004969_07	Continuation (8 of
c	40	17.2	74.8	110000	15	CP000086_20	Continuation (21 o
c	41	17.2	74.8	110000	15	CP000142_00	CP000142 Pelobacte
c	42	17.2	74.8	110000	15	RME591985_13	Continuation (14 o
	43	17.2	74.8	110807	6	AP003184	AP003184 Mus muscu
	44	17.2	74.8	135862	6	AC132576	AC132576 Mus muscu
	45	17.2	74.8	143895	4	CNS08CD6	AL954852 Oryza sat
	46	17.2	74.8	152191	4	AP005194	AP005194 Oryza sat
c	47	17.2	74.8	155094	12	AC122080	AC122080 Rattus no
	48	17.2	74.8	157990	12	AC137311	AC137311 Rattus no
	49	17.2	74.8	165518	13	AC091226	AC091226 Drosophil
c	50	17.2	74.8	171749	6	AC134437	AC134437 Mus muscu
c	51	17.2	74.8	177466	15	AE001826	AE001826 Deinococc
	52	17.2	74.8	191909	12	AC161801	AC161801 Mus muscu
c	53	17.2	74.8	193074	12	AC017576	AC017576 Drosophil
	54	17.2	74.8	203416	6	AC125352	AC125352 Mus muscu
c	55	17.2	74.8	217713	12	AC119007	AC119007 Rattus no
	56	17.2	74.8	238355	12	AC113917	AC113917 Rattus no

SCORE Search Results Details for Application 10 Result us-10-630-536-6.rng.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
start

```
                        GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        July  1, 2006, 03:53:57 ; Search time 138.66 Seconds
                                        (without alignments)
                                        1156.508 Million cell updates/sec

Title:         US-10-630-536-6
Perfect score: 23
Sequence:      1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:     10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :     N_Geneseq_8:*
               1:  geneseqn1980s:*
               2:  geneseqn1990s:*
               3:  geneseqn2000s:*
               4:  geneseqn2001as:*
               5:  geneseqn2001bs:*
               6:  geneseqn2002as:*
               7:  geneseqn2002bs:*
               8:  geneseqn2003as:*
               9:  geneseqn2003bs:*
               10:  geneseqn2003cs:*
               11:  geneseqn2003ds:*
               12:  geneseqn2004as:*
               13:  geneseqn2004bs:*
               14:  geneseqn2005s:*
               15:  geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23	100.0	23	14	ADV04871	Adv04871 Yersinia
c	2	23	100.0	147	14	ADV04873	Adv04873 Yersinia
	3	23	100.0	100990	12	ADJ94407	Adj94407 Yersinia
	4	17.8	77.4	1443	8	ACA41226	Aca41226 Prokaryot
	5	17.8	77.4	1443	10	ABZ39903	Abz39903 N. gonorr
	6	17.2	74.8	738	6	ABK77728	Abk77728 Bacillus
	7	17.2	74.8	1974	8	ACA40983	Aca40983 Prokaryot
	8	17.2	74.8	1974	10	ABZ40096	Abz40096 N. gonorr
	9	17.2	74.8	1977	8	ACA41918	Aca41918 Prokaryot
c	10	17.2	74.8	48275	3	AAA81501	Aaa81501 N. mening
c	11	17.2	74.8	56390	4	ABL22618	Abl22618 Drosophil
	12	17.2	74.8	110000	3	AAA81489_0	Aaa81489 N. mening
	13	17.2	74.8	349980	3	AAF21610	Aaf21610 Neisseria
	14	16.8	73.0	1404	6	ABN67300	Abn67300 Streptoco
	15	16.8	73.0	1404	6	ABN70378	Abn70378 Streptoco
	16	16.8	73.0	31122	2	AAQ40706	Aaq40706 Bacillus
c	17	16.8	73.0	110000	6	ABN71527_17	Continuation (18 o
c	18	16.8	73.0	110000	6	ABN71527_18	Continuation (19 o
	19	16.8	73.0	349980	6	ABQ81847	Abq81847 Bifidobac
c	20	16.6	72.2	25	9	ACK05770	Ack05770 Human mic
	21	16.6	72.2	30	13	ADS73313	Ads73313 Plant 3 R
c	22	16.6	72.2	333	6	ABN20453	Abn20453 Human ORF
c	23	16.6	72.2	337	6	ABN19524	Abn19524 Human ORF
c	24	16.6	72.2	363	5	ABV06373	Abv06373 Human pro
	25	16.6	72.2	378	11	ABD06655	Abd06655 Pseudomon
c	26	16.6	72.2	465	5	AAS79166	Aas79166 DNA encod
c	27	16.6	72.2	513	5	AAH65061	Aah65061 C glutami
c	28	16.6	72.2	636	14	AEB15370	Aeb15370 C glutami
c	29	16.6	72.2	636	14	AED72481	Aed72481 Corynebac
	30	16.6	72.2	834	12	ADO07789	Ado07789 Fly polyn
	31	16.6	72.2	981	11	ABD06627	Abd06627 Pseudomon
	32	16.6	72.2	1159	4	ABL18289	Abl18289 Drosophil
c	33	16.6	72.2	1275	4	AAF29692	Aaf29692 P acnes 1
c	34	16.6	72.2	1275	12	ADJ34080	Adj34080 P. acnes
c	35	16.6	72.2	1278	12	ADJ34074	Adj34074 P. acnes
	36	16.6	72.2	1650	5	AAS89367	Aas89367 DNA encod
c	37	16.6	72.2	1988	13	ADX51497	Adx51497 Plant ful
c	38	16.6	72.2	2028	10	ADE58576	Ade58576 Human gen
c	39	16.6	72.2	2172	14	ACL69720	Acl69720 M. xanthu
c	40	16.6	72.2	5275	4	AAF29691	Aaf29691 P acnes 1
	41	16.6	72.2	5801	4	AAS59582	Aas59582 Propionib
	42	16.6	72.2	5801	8	ACF64511	Acf64511 Propionib
c	43	16.6	72.2	11301	14	ACL64583	Acl64583 M. xanthu
	44	16.6	72.2	16658	4	AAS59630	Aas59630 Propionib
	45	16.6	72.2	16658	8	ACF64559	Acf64559 Propionib
c	46	16.6	72.2	34361	4	ABL18288	Abl18288 Drosophil
	47	16.6	72.2	349980	5	AAH64966	Aah64966 C glutami
c	48	16.4	71.3	109	2	AAX56039	Aax56039 HIV-1 Gro
c	49	16.4	71.3	109	2	AAX37154	Aax37154 PCR prime
c	50	16.4	71.3	109	3	AAZ90265	Aaz90265 Synthetic
c	51	16.4	71.3	1125	2	AAX56076	Aax56076 HIV-1 Gro
c	52	16.4	71.3	1125	2	AAX37191	Aax37191 Recombina
c	53	16.4	71.3	1860	2	AAX56077	Aax56077 HIV-1 Gro
c	54	16.4	71.3	1860	2	AAX37192	Aax37192 Recombina
c	55	16.4	71.3	1860	3	AAZ90283	Aaz90283 HIV-1 gro
	56	16.4	71.3	4073	12	ADQ64993	Adq64993 Novel hum

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-6.rr

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 536-6.rni.

start

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                         GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 04:28:37 ; Search time 28.2273 Seconds
                                          (without alignments)
                                          1524.607 Million cell updates/sec

Title:          US-10-630-536-6
Perfect score:  23
Sequence:       1 cgtcgatgactttctgacggcac 23

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:     2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      Issued_Patents_NA:*
                1:   /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                2:   /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                3:   /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                4:   /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                5:   /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                6:   /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                7:   /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                8:   /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                9:   /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result                 Query
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	No.	Score	Match	Length	DB	ID	Description
	1	23	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
	2	17.2	74.8	738	5	US-09-974-300-5019	Sequence 5019, Ap
c	3	16.8	73.0	69909	3	US-09-949-016-13423	Sequence 13423, A
	4	16.6	72.2	378	3	US-09-252-991A-5259	Sequence 5259, Ap
c	5	16.6	72.2	636	4	US-09-605-703B-2657	Sequence 2657, Ap
	6	16.6	72.2	640	3	US-09-270-767-15249	Sequence 15249, A
	7	16.6	72.2	981	3	US-09-252-991A-5231	Sequence 5231, Ap
c	8	16.6	72.2	1275	3	US-09-561-077C-60	Sequence 60, Appl
c	9	16.6	72.2	2172	3	US-09-902-540-6183	Sequence 6183, Ap
c	10	16.6	72.2	5275	3	US-09-561-077C-59	Sequence 59, Appl
c	11	16.6	72.2	11301	3	US-09-902-540-1046	Sequence 1046, Ap
c	12	16.4	71.3	109	2	US-08-912-129A-12	Sequence 12, Appl
c	13	16.4	71.3	109	3	US-08-911-824-12	Sequence 12, Appl
c	14	16.4	71.3	1125	2	US-08-912-129A-51	Sequence 51, Appl
c	15	16.4	71.3	1125	3	US-08-911-824-51	Sequence 51, Appl
c	16	16.4	71.3	1860	2	US-08-912-129A-53	Sequence 53, Appl
c	17	16.4	71.3	1860	3	US-08-911-824-53	Sequence 53, Appl
	18	16.2	70.4	228	3	US-09-248-796A-4395	Sequence 4395, Ap
	19	16.2	70.4	1008	3	US-09-106-075A-17	Sequence 17, Appl
	20	16.2	70.4	1068	2	US-08-210-762E-18	Sequence 18, Appl
	21	16.2	70.4	1191	2	US-08-210-762E-20	Sequence 20, Appl
	22	16.2	70.4	1191	3	US-09-106-075A-20	Sequence 20, Appl
c	23	16.2	70.4	1215	3	US-09-489-039A-2312	Sequence 2312, Ap
	24	16.2	70.4	1413	3	US-09-248-796A-4379	Sequence 4379, Ap
c	25	16.2	70.4	2334	3	US-09-248-796A-1911	Sequence 1911, Ap
	26	16.2	70.4	101674	3	US-09-949-016-12033	Sequence 12033, A
	27	15.8	68.7	2151	3	US-09-303-518D-111	Sequence 111, App
c	28	15.8	68.7	7029	5	US-10-261-481-1	Sequence 1, Appli
c	29	15.8	68.7	32155	3	US-08-311-731A-1	Sequence 1, Appli
	30	15.8	68.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	31	15.8	68.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	32	15.6	67.8	582	3	US-09-252-991A-12907	Sequence 12907, A
	33	15.6	67.8	601	3	US-09-949-016-200076	Sequence 200076,
	34	15.6	67.8	805	3	US-09-270-767-9873	Sequence 9873, Ap
c	35	15.6	67.8	1128	3	US-09-902-540-7183	Sequence 7183, Ap
	36	15.6	67.8	1149	3	US-09-303-518D-189	Sequence 189, App
	37	15.6	67.8	1149	3	US-09-303-518D-191	Sequence 191, App
	38	15.6	67.8	1275	3	US-09-107-532A-2687	Sequence 2687, Ap
	39	15.6	67.8	4094	3	US-09-902-540-665	Sequence 665, App
	40	15.6	67.8	22927	3	US-09-949-016-11849	Sequence 11849, A
	41	15.6	67.8	22928	3	US-09-949-016-13071	Sequence 13071, A
	42	15.6	67.8	36181	3	US-08-311-731A-120	Sequence 120, App
c	43	15.6	67.8	38653	3	US-09-922-445-1	Sequence 1, Appli
	44	15.6	67.8	84296	3	US-09-949-016-17375	Sequence 17375, A
	45	15.6	67.8	536165	3	US-09-214-808-1	Sequence 1, Appli
c	46	15.6	67.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	47	15.6	67.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	48	15.4	67.0	601	3	US-09-949-016-198698	Sequence 198698,
c	49	15.4	67.0	601	3	US-09-949-016-198699	Sequence 198699,
c	50	15.4	67.0	6944	3	US-09-949-016-3637	Sequence 3637, Ap
c	51	15.4	67.0	150597	3	US-09-949-016-15379	Sequence 15379, A
	52	15.4	67.0	767677	3	US-09-949-016-12147	Sequence 12147, A
	53	15.4	67.0	767677	3	US-09-949-016-17361	Sequence 17361, A
	54	15.2	66.1	25	3	US-09-396-196G-27431	Sequence 27431, A
	55	15.2	66.1	372	3	US-09-453-702B-33	Sequence 33, Appl
	56	15.2	66.1	372	3	US-10-114-170-33	Sequence 33, Appl
c	57	15.2	66.1	441	3	US-09-252-991A-6220	Sequence 6220, Ap
c	58	15.2	66.1	519	3	US-09-252-991A-7910	Sequence 7910, Ap
	59	15.2	66.1	529	3	US-09-533-559-4103	Sequence 4103, Ap

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-6.rn

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 6.rnpbm.

start

Go Back to pr

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                     GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:38:10 ; Search time 320.184 Seconds
                                          (without alignments)
                                          882.666 Million cell updates/sec

Title:           US-10-630-536-6
Perfect score:   23
Sequence:        1 cgtcgatgactttctgacggcac 23

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       Published_Applications_NA_Main:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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                 9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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                 14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23	100.0	23	11	US-10-630-536-6	Sequence 6, Appli
c	2	23	100.0	147	11	US-10-630-536-8	Sequence 8, Appli
	3	17.8	77.4	1443	8	US-10-282-122A-29096	Sequence 29096, A
	4	17.8	77.4	1443	10	US-10-467-657-4395	Sequence 4395, Ap
c	5	17.2	74.8	25	9	US-10-719-900-710490	Sequence 710490,
	6	17.2	74.8	738	3	US-09-974-300-5019	Sequence 5019, Ap
	7	17.2	74.8	1974	8	US-10-282-122A-28853	Sequence 28853, A
	8	17.2	74.8	1974	10	US-10-467-657-4781	Sequence 4781, Ap
	9	17.2	74.8	1977	8	US-10-282-122A-29788	Sequence 29788, A
c	10	17.2	74.8	48275	10	US-10-915-740A-48	Sequence 48, Appl
c	11	17.2	74.8	56390	13	US-11-097-143-31168	Sequence 31168, A
	12	17.2	74.8	2242716	10	US-10-915-740A-1068	Sequence 1068, Ap
	13	16.8	73.0	25	11	US-10-933-982-188166	Sequence 188166,
c	14	16.8	73.0	727	8	US-10-424-599-74159	Sequence 74159, A
	15	16.8	73.0	2256646	8	US-10-470-565-1	Sequence 1, Appli
c	16	16.6	72.2	25	6	US-10-098-263B-105751	Sequence 105751,
c	17	16.6	72.2	363	9	US-10-357-930-6364	Sequence 6364, Ap
c	18	16.6	72.2	465	10	US-10-450-763-14970	Sequence 14970, A
c	19	16.6	72.2	513	3	US-09-738-626-96	Sequence 96, Appl
	20	16.6	72.2	543	4	US-09-925-065A-883416	Sequence 883416,
	21	16.6	72.2	543	5	US-09-925-065A-883416	Sequence 883416,
c	22	16.6	72.2	636	13	US-11-006-098-285	Sequence 285, App
	23	16.6	72.2	834	8	US-10-267-502-115	Sequence 115, App
	24	16.6	72.2	1159	13	US-11-097-143-24674	Sequence 24674, A
c	25	16.6	72.2	1275	9	US-10-755-087-60	Sequence 60, Appl
	26	16.6	72.2	1650	10	US-10-450-763-25171	Sequence 25171, A
c	27	16.6	72.2	1988	8	US-10-425-114-26237	Sequence 26237, A
c	28	16.6	72.2	5275	9	US-10-755-087-59	Sequence 59, Appl
c	29	16.6	72.2	34361	13	US-11-097-143-24673	Sequence 24673, A
	30	16.6	72.2	3309400	3	US-09-738-626-1	Sequence 1, Appli
c	31	16.4	71.3	109	2	US-08-911-824-12	Sequence 12, Appl
c	32	16.4	71.3	642	12	US-10-301-480-347442	Sequence 347442,
c	33	16.4	71.3	642	12	US-10-301-480-960851	Sequence 960851,
c	34	16.4	71.3	643	4	US-09-925-065A-269906	Sequence 269906,
c	35	16.4	71.3	643	5	US-09-925-065A-269906	Sequence 269906,
c	36	16.4	71.3	1125	2	US-08-911-824-51	Sequence 51, Appl
	37	16.4	71.3	1696	10	US-10-750-185-58729	Sequence 58729, A
	38	16.4	71.3	1696	10	US-10-750-623-58729	Sequence 58729, A
c	39	16.4	71.3	1860	2	US-08-911-824-53	Sequence 53, Appl
	40	16.4	71.3	7500	8	US-10-468-027-1	Sequence 1, Appli
	41	16.4	71.3	7506	3	US-09-815-379-7	Sequence 7, Appli
	42	16.4	71.3	7506	16	US-11-285-818-7	Sequence 7, Appli
	43	16.2	70.4	263	9	US-10-425-115-120427	Sequence 120427,
c	44	16.2	70.4	546	4	US-09-925-065A-282231	Sequence 282231,
c	45	16.2	70.4	546	4	US-09-925-065A-282232	Sequence 282232,
c	46	16.2	70.4	546	5	US-09-925-065A-282231	Sequence 282231,
c	47	16.2	70.4	546	5	US-09-925-065A-282232	Sequence 282232,
c	48	16.2	70.4	554	12	US-10-301-480-359156	Sequence 359156,
c	49	16.2	70.4	554	12	US-10-301-480-359157	Sequence 359157,
c	50	16.2	70.4	554	12	US-10-301-480-972565	Sequence 972565,
c	51	16.2	70.4	554	12	US-10-301-480-972566	Sequence 972566,
	52	16.2	70.4	559	8	US-10-767-701-316	Sequence 316, App
	53	16.2	70.4	590	3	US-09-925-298-194	Sequence 194, App
	54	16.2	70.4	590	6	US-10-102-806-194	Sequence 194, App

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-6.rn

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
6.rnpbn.

start

Go Back to prev

```
                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 04:39:12 ; Search time 23.8804 Seconds
                                         (without alignments)
                                         1138.902 Million cell updates/sec

Title:          US-10-630-536-6
Perfect score:  23
Sequence:       1 cgtcgatgactttctgacggcac 23

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters:      1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      Published_Applications_NA_New:*
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                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17.4	75.7	1432	6	US-10-449-902-9967	Sequence 9967, Ap

	2	16.6	72.2	30	6	US-10-548-484-47	Sequence 47, Appl
c	3	16.4	71.3	1000	7	US-11-266-748A-197438	Sequence 197438,
	4	16.2	70.4	599	7	US-11-266-748A-13758	Sequence 13758, A
	5	16.2	70.4	599	7	US-11-266-748A-176891	Sequence 176891,
	6	16.2	70.4	599	7	US-11-266-748A-249917	Sequence 249917,
c	7	16.2	70.4	599	7	US-11-266-748A-310434	Sequence 310434,
	8	16.2	70.4	623	7	US-11-266-748A-82480	Sequence 82480, A
c	9	16.2	70.4	623	7	US-11-266-748A-135291	Sequence 135291,
	10	16.2	70.4	750	7	US-11-266-748A-286458	Sequence 286458,
c	11	16.2	70.4	750	7	US-11-266-748A-337887	Sequence 337887,
	12	16.2	70.4	750	7	US-11-266-748A-396917	Sequence 396917,
c	13	16.2	70.4	750	7	US-11-266-748A-467963	Sequence 467963,
c	14	16.2	70.4	1968	7	US-11-217-529-1728	Sequence 1728, Ap
c	15	16.2	70.4	5642	7	US-11-266-748A-28401	Sequence 28401, A
	16	15.8	68.7	139515	7	US-11-266-748A-59425	Sequence 59425, A
	17	15.6	67.8	863	6	US-10-449-902-7490	Sequence 7490, Ap
c	18	15.6	67.8	1118	7	US-11-266-748A-171217	Sequence 171217,
	19	15.6	67.8	1406	6	US-10-449-902-3044	Sequence 3044, Ap
	20	15.6	67.8	1933	6	US-10-449-902-14182	Sequence 14182, A
	21	15.6	67.8	1940	6	US-10-449-902-24465	Sequence 24465, A
	22	15.6	67.8	2534	6	US-10-449-902-20488	Sequence 20488, A
	23	15.6	67.8	4018	6	US-10-449-902-15709	Sequence 15709, A
c	24	15.4	67.0	664	7	US-11-266-748A-16575	Sequence 16575, A
c	25	15.4	67.0	780	7	US-11-266-748A-51263	Sequence 51263, A
c	26	15.4	67.0	839	7	US-11-266-748A-53185	Sequence 53185, A
	27	15.4	67.0	911	7	US-11-266-748A-164942	Sequence 164942,
c	28	15.4	67.0	919	7	US-11-266-748A-5978	Sequence 5978, Ap
c	29	15.4	67.0	1291	7	US-11-266-748A-226775	Sequence 226775,
c	30	15.4	67.0	2378	7	US-11-266-748A-76596	Sequence 76596, A
	31	15.4	67.0	2378	7	US-11-266-748A-129407	Sequence 129407,
	32	15.2	66.1	25	7	US-11-217-529-157618	Sequence 157618,
c	33	15.2	66.1	383	7	US-11-266-748A-419015	Sequence 419015,
c	34	15.2	66.1	440	6	US-10-953-349-5917	Sequence 5917, Ap
c	35	15.2	66.1	480	7	US-11-266-748A-231028	Sequence 231028,
	36	15.2	66.1	690	7	US-11-217-529-82027	Sequence 82027, A
	37	15.2	66.1	822	6	US-10-471-571A-2345	Sequence 2345, Ap
	38	15.2	66.1	977	6	US-10-953-349-38966	Sequence 38966, A
c	39	15.2	66.1	1000	7	US-11-266-748A-195958	Sequence 195958,
	40	15.2	66.1	1000	7	US-11-266-748A-408223	Sequence 408223,
c	41	15.2	66.1	1000	7	US-11-266-748A-479269	Sequence 479269,
c	42	15.2	66.1	1029	6	US-10-449-902-4545	Sequence 4545, Ap
c	43	15.2	66.1	1252	6	US-10-449-902-15361	Sequence 15361, A
c	44	15.2	66.1	1319	6	US-10-449-902-13341	Sequence 13341, A
c	45	15.2	66.1	1356	7	US-11-217-529-77511	Sequence 77511, A
	46	15.2	66.1	1430	6	US-10-449-902-28031	Sequence 28031, A
c	47	15.2	66.1	2067	7	US-11-217-529-1780	Sequence 1780, Ap
	48	15.2	66.1	2370	7	US-11-217-529-3430	Sequence 3430, Ap
	49	15.2	66.1	2721	6	US-10-449-902-25970	Sequence 25970, A
	50	15.2	66.1	3219	7	US-11-217-529-79	Sequence 79, Appl
c	51	15.2	66.1	3544	7	US-11-266-748A-60407	Sequence 60407, A
c	52	15.2	66.1	3653	7	US-11-266-748A-23838	Sequence 23838, A
c	53	15.2	66.1	162354	7	US-11-266-748A-23437	Sequence 23437, A
c	54	15	65.2	501	7	US-11-266-748A-373946	Sequence 373946,
	55	15	65.2	501	7	US-11-266-748A-457325	Sequence 457325,
c	56	15	65.2	667	6	US-10-953-349-29188	Sequence 29188, A
	57	15	65.2	781	6	US-10-449-902-7495	Sequence 7495, Ap
c	58	15	65.2	1113	7	US-11-217-529-2143	Sequence 2143, Ap
	59	15	65.2	1200	6	US-10-513-951-1	Sequence 1, Appli
c	60	15	65.2	1263	6	US-10-953-349-24782	Sequence 24782, A
c	61	15	65.2	1342	6	US-10-449-902-13269	Sequence 13269, A
c	62	15	65.2	1351	6	US-10-449-902-15822	Sequence 15822, A

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-6.rst.

<u>Score Home Page</u>   <u>Retrieve Application List</u>   <u>SCORE System Overview</u>   <u>SCORE FAQ</u>   <u>Comments / Suggestions</u>

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-6.rst.

<u>start</u>

<u>Go Back to previous page</u>

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                        GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:           July 1, 2006, 04:17:07 ; Search time 834.328 Seconds
                                          (without alignments)
                                          1541.534 Million cell updates/sec

Title:            US-10-630-536-6
Perfect score:    23
Sequence:         1 cgtcgatgactttctgacggcac 23

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:    96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :        EST:*
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                  2:  gb_est3:*
                  3:  gb_est4:*
                  4:  gb_est5:*
                  5:  gb_est6:*
                  6:  gb_htc:*
                  7:  gb_est2:*
                  8:  gb_est7:*
                  9:  gb_est8:*
                  10:  gb_est9:*
                  11:  gb_gss1:*
                  12:  gb_gss2:*
                  13:  gb_gss3:*
                  14:  gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18.8	81.7	843	2	BI552452	BI552452 603196152
c	2	18.4	80.0	828	13	CW701834	CW701834 AIAA-aaa7
c	3	18.2	79.1	584	3	BM610335	BM610335 170006871
	4	18.2	79.1	659	8	CV749968	CV749968 SJL2-006_
c	5	18.2	79.1	683	3	BM595095	BM595095 170006874
c	6	18.2	79.1	763	4	BX606660	BX606660 BX606660
c	7	18.2	79.1	806	13	CL740054	CL740054 OR_BBa007
	8	18.2	79.1	924	8	CV455016	CV455016 EST908925
	9	18	78.3	667	10	DT123661	DT123661 JGI_ANNO8
	10	17.8	77.4	516	13	CZ677176	CZ677176 OM_Ba023
c	11	17.8	77.4	525	13	CZ058768	CZ058768 OM_Ba005
	12	17.8	77.4	597	11	AQ991590	AQ991590 Rfc02585
	13	17.8	77.4	658	3	BQ414930	BQ414930 GA__Ed009
c	14	17.8	77.4	669	9	DN382728	DN382728 LIB38534_
	15	17.8	77.4	672	3	BQ415082	BQ415082 GA__Ed009
c	16	17.8	77.4	689	13	CZ084706	CZ084706 OM_Ba008
c	17	17.8	77.4	810	10	DT207923	DT207923 JGI_CAAS1
	18	17.8	77.4	826	10	DT466964	DT466964 GH_CHX19K
	19	17.8	77.4	869	14	AG839434	AG839434 Oryza sat
	20	17.6	76.5	1012	4	BX398870	BX398870 BX398870
	21	17.4	75.7	774	12	CG178031	CG178031 PUIMG92TB
	22	17.4	75.7	862	12	CG145737	CG145737 PUIFI37TD
c	23	17.2	74.8	234	5	CK744115	CK744115 ltu01-17m
	24	17.2	74.8	398	9	CX619746	CX619746 GABR1_47_
c	25	17.2	74.8	507	2	BI377699	BI377699 BFLG3_001
	26	17.2	74.8	532	10	DW567646	DW567646 EST_ssal_
	27	17.2	74.8	542	10	DT710673	DT710673 s13dFA40E
c	28	17.2	74.8	573	2	BI380338	BI380338 BFLG1_001
	29	17.2	74.8	583	10	DT710719	DT710719 s13dFA39B
c	30	17.2	74.8	585	4	CA020194	CA020194 HV14J20r
c	31	17.2	74.8	624	5	CF396743	CF396743 RTDS2_24_
c	32	17.2	74.8	629	12	CE774610	CE774610 tigr-gss-
	33	17.2	74.8	640	10	DT703147	DT703147 s13dFA34E
	34	17.2	74.8	666	14	AG944174	AG944174 Drosophil
	35	17.2	74.8	684	8	CO817802	CO817802 FA_SEa001
c	36	17.2	74.8	741	4	CA056306	CA056306 ssalrgb50
c	37	17.2	74.8	744	10	DT806162	DT806162 Hh_emG_06
c	38	17.2	74.8	776	14	AG053067	AG053067 Pan trogl
	39	17.2	74.8	795	5	CK177973	CK177973 EST767293
c	40	17.2	74.8	797	12	BZ975468	BZ975468 PUFJU69TD
c	41	17.2	74.8	829	5	CK177972	CK177972 EST767292
	42	17.2	74.8	836	14	DU870542	DU870542 98858 Tom
c	43	17.2	74.8	859	14	CR245554	CR245554 Forward s
c	44	17.2	74.8	870	8	CN168957	CN168957 AGENCOURT
c	45	17.2	74.8	905	11	BH401834	BH401834 AG-ND-149
c	46	17.2	74.8	930	7	BE270919	BE270919 600943796
	47	17.2	74.8	953	3	BQ070370	BQ070370 AGENCOURT
	48	17.2	74.8	968	14	DU859776	DU859776 65066 Tom
	49	17.2	74.8	1021	4	BX339220	BX339220 BX339220
	50	17.2	74.8	1365	14	AJ858811	AJ858811 Brassica
	51	17.2	74.8	1593	7	BF664382	BF664382 602146044
c	52	17.2	74.8	1998	6	CNS0AE0I	BX815525 Arabidops
	53	17	73.9	560	9	DB277756	DB277756 DB277756

SCORE Search Results Details for Application 10 630-536-7.rge

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:

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                        GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 03:55:42 ; Search time 491.763 Seconds
                                         (without alignments)
                                         4291.222 Million cell updates/sec

Title:          US-10-630-536-7
Perfect score:  33
Sequence:       1 cgagatagccctgataacgcttcacagtatggc 33

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:       12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
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                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
                10:  gb_vi:*
                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	33	100.0	33	2	CS001826	CS001826 Sequence
	2	33	100.0	147	2	CS001827	CS001827 Sequence
	3	33	100.0	96210	15	YPPMT1	AL117211 Yersinia
	4	33	100.0	100984	15	AF053947	AF053947 Yersinia
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ALIGNMENTS


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DEFINITION    Sequence 7 from Patent WO2004106553.
ACCESSION     CS001826
VERSION       CS001826.1  GI:58424081
KEYWORDS      .
SOURCE        Yersinia pestis
  ORGANISM    Yersinia pestis
              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
              Enterobacteriaceae; Yersinia.
REFERENCE     1
  AUTHORS     McCready,P.M., Radnedge,L., Andersen,G.L., Ott,L.L., Slezak,T.R.,
              Kuczmarski,T.A. and Motin,V.L.
  TITLE       Nucleotide sequences specific to Yersinia pestis and methods for
              the detection of Yersinia pestis
  JOURNAL     Patent: WO 2004106553-A 7 09-DEC-2004;
              The Regents of The University of California (US)
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SCORE Search Results Details for Application 10 Search Result us-10-630-536-7.rng.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:

start

Gc

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        July  1, 2006, 03:53:57 ; Search time 198.947 Seconds
                                         (without alignments)
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Title:         US-10-630-536-7
Perfect score: 33
Sequence:      1 cgagatagccctgataacgcttcacagtatggc 33

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

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     Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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	100	17.8	53.9	633	2	AAV24733	Aav24733 H. pylori
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	103	17.8	53.9	681	13	ADQ48797	Adq48797 Novel can
c	104	17.8	53.9	698	13	ADX35473	Adx35473 Plant ful
c	105	17.8	53.9	726	13	ADX09418	Adx09418 Plant ful
	106	17.8	53.9	774	2	AAV24871	Aav24871 H. pylori
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c	109	17.8	53.9	1195	13	ADX51605	Adx51605 Plant ful
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	111	17.8	53.9	1251	14	ADZ38635	Adz38635 Group A S
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c	113	17.8	53.9	1364	13	ADX12861	Adx12861 Plant ful
	114	17.8	53.9	1555	13	ADX09668	Adx09668 Plant ful
c	115	17.8	53.9	1646	13	ADT19108	Adt19108 Plant cDN
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SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-7.r

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6: 7.rni.

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OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 04:28:37 ; Search time 40.5 Seconds
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Total number of hits satisfying chosen parameters:     2807332

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Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a
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                                SUMMARIES
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7.rnpbm.

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	48	18.6	56.4	2921	10	US-10-450-763-10541	Sequence 10541, A
	49	18.6	56.4	3470	9	US-10-357-930-25055	Sequence 25055, A
	50	18.6	56.4	4502	10	US-10-450-763-22530	Sequence 22530, A
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	52	18.4	55.8	293	4	US-09-925-065A-494611	Sequence 494611,
	53	18.4	55.8	293	5	US-09-925-065A-494611	Sequence 494611,
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c	57	18.4	55.8	600	10	US-10-972-079-78001	Sequence 78001, A
	58	18.4	55.8	637	4	US-09-925-065A-516799	Sequence 516799,
	59	18.4	55.8	637	4	US-09-925-065A-516800	Sequence 516800,
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	62	18.4	55.8	1000	10	US-10-868-397-469	Sequence 469, App
	63	18.4	55.8	1216	3	US-09-764-891-1350	Sequence 1350, Ap
	64	18.4	55.8	24515	13	US-11-097-143-9910	Sequence 9910, Ap
	65	18.4	55.8	25381	13	US-11-097-143-9364	Sequence 9364, Ap
c	66	18.4	55.8	135462	11	US-10-330-773-37	Sequence 37, Appl
	67	18.4	55.8	1691139	6	US-10-067-514-1	Sequence 1, Appli
	68	18.4	55.8	1691139	8	US-10-419-723-1	Sequence 1, Appli
	69	18.4	55.8	1691139	8	US-10-255-120-1	Sequence 1, Appli
	70	18.4	55.8	1691140	10	US-10-868-397-1	Sequence 1, Appli
	71	18.4	55.8	1691140	15	US-11-091-018-1	Sequence 1, Appli
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c	74	18.2	55.2	201	9	US-10-741-600-39029	Sequence 39029, A
	75	18.2	55.2	201	9	US-10-741-600-47660	Sequence 47660, A
	76	18.2	55.2	201	10	US-10-995-561-51898	Sequence 51898, A
	77	18.2	55.2	219	6	US-10-096-986-86	Sequence 86, Appl
c	78	18.2	55.2	545	4	US-09-925-065A-443369	Sequence 443369,
c	79	18.2	55.2	545	5	US-09-925-065A-443369	Sequence 443369,
	80	18.2	55.2	555	7	US-10-369-493-25426	Sequence 25426, A
	81	18.2	55.2	555	11	US-10-932-182A-76293	Sequence 76293, A
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	86	18.2	55.2	584	12	US-10-301-480-503807	Sequence 503807,
	87	18.2	55.2	584	12	US-10-301-480-1117216	Sequence 1117216,
c	88	18.2	55.2	596	12	US-10-301-480-372809	Sequence 372809,
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	115	18	54.5	299	8	US-10-424-599-123985	Sequence 123985,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-7.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:39:12 ; Search time 34.2632 Seconds
                                          (without alignments)
                                          1138.902 Million cell updates/sec

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Perfect score:   33
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters:      1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result          Query
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	7	18.6	56.4	2919	7	US-11-266-748A-29636	Sequence 29636, A
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	25	17.8	53.9	261789	7	US-11-260-842-1	Sequence 1, Appli
	26	17.6	53.3	310	7	US-11-266-748A-269400	Sequence 269400,
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c	30	17.6	53.3	1481	7	US-11-216-545-7597	Sequence 7597, Ap
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	37	17.6	53.3	2488	7	US-11-266-748A-57615	Sequence 57615, A
	38	17.6	53.3	2739	7	US-11-266-748A-56100	Sequence 56100, A
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	47	17.4	52.7	1438	7	US-11-266-748A-168317	Sequence 168317,
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SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-7.rst.

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:17:07 ; Search time 1197.08 Seconds
                                          (without alignments)
                                          1541.534 Million cell updates/sec

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Total number of hits satisfying chosen parameters:      96473596

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	22.6	68.5	775	3	BW079729	BW079729 BW079729
	4	21.4	64.8	867	8	CX014404	CX014404 io70f11.g
c	5	21	63.6	318	7	AV892330	AV892330 AV892330
c	6	21	63.6	392	7	AV892476	AV892476 AV892476
c	7	21	63.6	513	3	BP022696	BP022696 BP022696
c	8	21	63.6	567	7	AV892305	AV892305 AV892305
c	9	21	63.6	596	7	AV892386	AV892386 AV892386
c	10	21	63.6	659	3	BW156906	BW156906 BW156906
c	11	21	63.6	668	3	BW234446	BW234446 BW234446
	12	21	63.6	670	2	BJ734845	BJ734845 BJ734845
	13	21	63.6	676	5	CD306405	CD306405 StrPu691.
	14	21	63.6	690	2	BJ705420	BJ705420 BJ705420
	15	21	63.6	694	2	BJ738061	BJ738061 BJ738061
c	16	21	63.6	695	7	AV892923	AV892923 AV892923
	17	21	63.6	703	2	BJ709530	BJ709530 BJ709530
	18	21	63.6	704	2	BJ527686	BJ527686 BJ527686
	19	21	63.6	721	2	BJ708080	BJ708080 BJ708080
	20	21	63.6	722	2	BJ713261	BJ713261 BJ713261
c	21	21	63.6	725	3	BW377887	BW377887 BW377887
c	22	21	63.6	728	3	BW084457	BW084457 BW084457
c	23	21	63.6	728	7	AV892276	AV892276 AV892276
c	24	21	63.6	728	7	AV892495	AV892495 AV892495
c	25	21	63.6	738	3	BW082867	BW082867 BW082867
c	26	21	63.6	738	3	BW102440	BW102440 BW102440
c	27	21	63.6	752	3	BW111676	BW111676 BW111676
c	28	21	63.6	776	3	BW421668	BW421668 BW421668
c	29	21	63.6	783	7	AV850207	AV850207 AV850207
c	30	21	63.6	807	12	CG309824	CG309824 OG3DO96TH
	31	21	63.6	812	2	BJ715326	BJ715326 BJ715326
c	32	21	63.6	874	12	CG213700	CG213700 OG3AH20TH
	33	21	63.6	933	12	CG309836	CG309836 OG3DO96TV
	34	21	63.6	1007	12	CG213708	CG213708 OG3AH20TV
	35	20.8	63.0	386	14	BX142971	BX142971 Danio rer
	36	20.8	63.0	466	11	AQ245808	AQ245808 HS_2058_A
	37	20.8	63.0	472	7	BF152282	BF152282 uz31c07.y
c	38	20.8	63.0	555	11	AZ379939	AZ379939 1M0135J11
	39	20.8	63.0	616	8	CV788229	CV788229 zaa60f10.
c	40	20.6	62.4	664	13	DU190643	DU190643 109853816
c	41	20.4	61.8	543	4	CA005709	CA005709 HU08P18u
	42	20.4	61.8	572	4	CA007777	CA007777 HU08P18r
	43	20.4	61.8	960	14	DU786754	DU786754 APKH1780.
	44	20.4	61.8	1147	9	DR154160	DR154160 49169271
	45	20.2	61.2	351	2	BM383354	BM383354 UI-R-DM1-
c	46	20.2	61.2	396	10	DR910548	DR910548 USDA-FP_1
c	47	20.2	61.2	520	7	BE566800	BE566800 601339793
c	48	20.2	61.2	584	5	CD334344	CD334344 StrPu536.
	49	20.2	61.2	739	8	CV708636	CV708636 UCRPT01_0
c	50	20.2	61.2	860	14	CR216782	CR216782 Forward s
	51	20.2	61.2	886	2	BI646005	BI646005 603274987
	52	20.2	61.2	957	5	CF814561	CF814561 EST691943
c	53	20.2	61.2	990	12	CL070841	CL070841 CH216-119

	54	20	60.6	237	1	AV292963	AV292963 AV292963
	55	20	60.6	516	11	AZ929176	AZ929176 479.dif23
c	56	20	60.6	892	10	DT795860	DT795860 126466490
	57	20	60.6	952	5	CF223182	CF223182 AGENCOURT
c	58	20	60.6	1290	10	DT774175	DT774175 107518310
	59	19.8	60.0	187	2	BI452378	BI452378 GI09_G04
	60	19.8	60.0	420	7	AW862434	AW862434 RC0-CT038
	61	19.8	60.0	456	14	DX237573	DX237573 OR_ABa012
	62	19.8	60.0	483	4	CD143635	CD143635 MG1-0086T
	63	19.8	60.0	572	5	CF210095	CF210095 CAB20005_
	64	19.8	60.0	632	3	BU998355	BU998355 HI10M16r
c	65	19.8	60.0	709	8	CV710829	CV710829 UCRPT01_0
c	66	19.8	60.0	713	9	CX542612	CX542612 UCRPT01_5
	67	19.8	60.0	754	14	AG508862	AG508862 Mus muscu
c	68	19.8	60.0	792	5	CK632917	CK632917 AM2-AP001
c	69	19.8	60.0	820	10	DV097575	DV097575 ppa01-71t
c	70	19.8	60.0	835	7	BF626518	BF626518 HVSMEa001
	71	19.8	60.0	840	2	BM020384	BM020384 603649030
c	72	19.8	60.0	868	5	CD573706	CD573706 UCRPT01_0
	73	19.8	60.0	948	4	CB275296	CB275296 6HRm257_6
c	74	19.8	60.0	992	12	CC190253	CC190253 CH261-37J
c	75	19.8	60.0	994	4	BX377561	BX377561 BX377561
	76	19.8	60.0	1114	10	DW027961	DW027961 CFW242-F0
	77	19.8	60.0	1305	9	DN711146	DN711146 CLJ93-E08
	78	19.8	60.0	1331	9	DN715403	DN715403 CNB108-A1
	79	19.8	60.0	1407	13	CL647804	CL647804 CH213-150
	80	19.8	60.0	1418	9	DN700227	DN700227 CLJ28-D08
	81	19.8	60.0	1423	9	DN715129	DN715129 CNB106-E0
c	82	19.6	59.4	342	1	AV693944	AV693944 AV693944
	83	19.6	59.4	381	4	BY670926	BY670926 BY670926
	84	19.6	59.4	420	11	BH406381	BH406381 RPCI-23-4
	85	19.6	59.4	427	7	AW390452	AW390452 RC3-ST018
c	86	19.6	59.4	452	3	BQ825770	BQ825770 1030129H0
	87	19.6	59.4	454	3	BQ825771	BQ825771 1030129H0
	88	19.6	59.4	488	11	AZ695864	AZ695864 RPCI-23-2
	89	19.6	59.4	584	11	AZ096654	AZ096654 RPCI-23-1
	90	19.6	59.4	635	11	AZ069345	AZ069345 RPCI-23-4
c	91	19.6	59.4	685	1	AB072941	AB072941 AB072941
	92	19.6	59.4	720	11	AZ246522	AZ246522 RPCI-23-9
	93	19.6	59.4	721	14	AG330283	AG330283 Mus muscu
	94	19.6	59.4	748	14	AG527571	AG527571 Mus muscu
	95	19.6	59.4	1047	3	BQ924279	BQ924279 AGENCOURT
c	96	19.6	59.4	3947	6	AK034463	AK034463 Mus muscu
c	97	19.4	58.8	228	7	BB302417	BB302417 BB302417
c	98	19.4	58.8	305	14	CR018870	CR018870 Forward s
c	99	19.4	58.8	378	2	BJ267217	BJ267217 BJ267217
c	100	19.4	58.8	380	7	BF249925	BF249925 pa88d07.y
c	101	19.4	58.8	401	2	BJ267420	BJ267420 BJ267420
	102	19.4	58.8	412	11	AQ030694	AQ030694 HS_2192_A
c	103	19.4	58.8	427	4	BY679318	BY679318 BY679318
c	104	19.4	58.8	489	4	CB893264	CB893264 EST646056
	105	19.4	58.8	494	11	AZ074221	AZ074221 RPCI-23-3
c	106	19.4	58.8	497	7	BF250836	BF250836 pb04h11.y
c	107	19.4	58.8	542	7	BE515541	BE515541 WHE0614_E
	108	19.4	58.8	542	8	CO529360	CO529360 3530_1_19
	109	19.4	58.8	559	9	DA930011	DA930011 DA930011
	110	19.4	58.8	574	9	DA046585	DA046585 DA046585
	111	19.4	58.8	585	5	CF255276	CF255276 mdvn126_c
	112	19.4	58.8	587	11	AZ277774	AZ277774 RPCI-23-1
c	113	19.4	58.8	602	2	BJ270750	BJ270750 BJ270750
c	114	19.4	58.8	623	2	BM138015	BM138015 WHE0479_D

SCORE Search Results Details for Application 10 630-536-8.rge

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:

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                        GenCore version 5.1.9
               Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 03:55:42 ; Search time 2190.58 Seconds
                                           (without alignments)
                                           4291.222 Million cell updates/sec

Title:           US-10-630-536-8
Perfect score:   147
Sequence:        1 atttgtcggaaggtcgcagt..........ccgtcagaaagtcatcgacg 147

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

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                                    SUMMARIES
                  %
Result          Query
    No.   Score  Match  Length DB  ID                     Description
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      1    147   100.0     147  2  CS001827               CS001827 Sequence
      2    147   100.0   96210 15  YPPMT1                  AL117211 Yersinia
      3    147   100.0  100984 15  AF053947                AF053947 Yersinia
c     4    147   100.0  100990  2  AR487637               AR487637 Sequence
c     5    147   100.0  100990 15  AF074611                AF074611 Yersinia
      6    147   100.0  106642 15  AE017045                AE017045 Yersinia
      7    147   100.0  137036 15  AJ698720                AJ698720 Yersinia
      8  142.2    96.7  106516 15  STYPPHCM2               AL513384 Salmonell
c     9     35    23.8  110000  4  CR382130_22            Continuation (23 o
     10     33    22.4      33  2  CS001826               CS001826 Sequence
c    11     32    21.8  110000 15  CR522870_30             Continuation (31 o
c    12   31.8    21.6   87538  5  AL158200               AL158200 Human DNA
     13   31.8    21.6  110000 15  CP000086_02             Continuation (3 of
c    14   31.8    21.6  110000 15  CP000110_22             Continuation (23 o
c    15   31.8    21.6  167498 12  AC156781               AC156781 Rhinoloph
     16   31.8    21.6  168235 12  AC166859                AC166859 Oryctolag
     17   31.8    21.6  180429 12  AC165394                AC165394 Oryctolag
c    18   31.6    21.5    1640  2  I08235                 I08235 Sequence 1
c    19   31.6    21.5    1640  2  I08236                 I08236 Sequence 2
     20   31.6    21.5    1643 15  INS493STY               M28508 Insertion e
     21   31.6    21.5   10478 15  AE012341                AE012341 Xanthomon
c    22   31.6    21.5  110000 15  CP000050_21            Continuation (22 o
c    23   31.6    21.5  132016 12  AC148128               AC148128 Ornithorh
c    24   31.4    21.4    2364 15  STMSSPP                 L76204 Streptomyce
c    25     31    21.1  234117 12  AC130985               AC130985 Rattus no
c    26   30.8    21.0    8507 13  DME010298               AJ010298 Drosophil
c    27   30.8    21.0   65557 12  AC010062               AC010062 Drosophil
c    28   30.8    21.0  110000 15  AE016827_04             Continuation (5 of
c    29   30.8    21.0  123010 12  AC009746               AC009746 Drosophil
     30   30.8    21.0  169021 13  CP000206               CP000206 Drosophil
c    31   30.8    21.0  189893 12  AC013254               AC013254 Drosophil
c    32   30.8    21.0  190289 10  MCU60315                U60315 Molluscum c
c    33   30.8    21.0  201451 12  AC013831               AC013831 Drosophil
c    34   30.6    20.8     913  7  BV467756               BV467756 G591P6008
     35   30.6    20.8  274094 12  AC163465                AC163465 Bos tauru
     36   30.4    20.7  110000 15  CP000090_30             Continuation (31 o
     37   30.4    20.7  150494  6  AC091617               AC091617 Rattus no
c    38   30.4    20.7  167694 12  CT033816                CT033816 Danio rer
c    39   30.4    20.7  169938 12  AC167145                AC167145 Bos tauru
c    40   30.4    20.7  185266 11  BX511261                BX511261 Zebrafish
c    41   30.4    20.7  197473 11  BX247866                BX247866 Zebrafish
c    42   30.4    20.7  241486 12  AC112561                AC112561 Rattus no
c    43   30.4    20.7  269708 12  AC097787                AC097787 Rattus no
c    44   30.4    20.7  289209 12  AC127408                AC127408 Rattus no
c    45   30.2    20.5   13360 15  AE005797                AE005797 Caulobact
c    46   30.2    20.5   72609  4  CR382129_32            Continuation (33 o
c    47   30.2    20.5  110000  4  CR382129_31            Continuation (32 o
     48   30.2    20.5  110000 15  BA000040_08             Continuation (9 of
     49   30.2    20.5  232636 12  CR931783                CR931783 Danio rer
     50     30    20.4    1119  2  AX652911               AX652911 Sequence
     51     30    20.4    1268  4  AY344487               AY344487 Oryza sat
     52     30    20.4    1310  4  AY323488               AY323488 Oryza sat
     53     30    20.4    1955  4  AK101824               AK101824 Oryza sat
     54     30    20.4    7306 12  AC015067               AC015067 Drosophil
     55     30    20.4  100168  4  AP003826               AP003826 Oryza sat
     56     30    20.4  110000  4  AP008213_041            Continuation (42 o
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c	57	30	20.4	121474	12	AC007150	AC007150 Drosophil
c	58	30	20.4	153484	12	AC160218	AC160218 Atelerix
	59	30	20.4	156063	12	AC146732	AC146732 Otolemur
	60	30	20.4	156691	11	BX914195	BX914195 Zebrafish
c	61	30	20.4	163162	13	AC006247	AC006247 Drosophil
c	62	30	20.4	164900	12	AC175627	AC175627 Atelerix
c	63	30	20.4	175868	12	AC113565	AC113565 Canis fam
	64	30	20.4	179545	12	AC146737	AC146737 Otolemur
	65	30	20.4	221945	13	AE003819	AE003819 Drosophil
c	66	29.8	20.3	1860	2	AR384175	AR384175 Sequence
c	67	29.8	20.3	7944	15	AB040071	AB040071 Streptomy
	68	29.8	20.3	110000	12	AP006493_0	AP006493 Cyanidios
	69	29.8	20.3	159872	12	CR931724	CR931724 Danio rer
c	70	29.6	20.1	1038	1	AY836625	AY836625 Unculture
c	71	29.6	20.1	1062	2	AR625957	AR625957 Sequence
c	72	29.6	20.1	2454	4	AF022816	AF022816 Chlamydom
	73	29.6	20.1	5467	2	AR619308	AR619308 Sequence
c	74	29.6	20.1	110000	15	CP000151_28	Continuation (29 o
c	75	29.6	20.1	110000	15	AE014184_06	Continuation (7 of
	76	29.6	20.1	173988	12	AC166210	AC166210 Oryctolag
	77	29.6	20.1	187110	6	AC131303	AC131303 Mus muscu
c	78	29.6	20.1	189349	12	AC174410	AC174410 Oryctolag
	79	29.6	20.1	192016	6	AC099582	AC099582 Mus muscu
	80	29.6	20.1	200904	11	CR376854	CR376854 Zebrafish
	81	29.6	20.1	201352	12	AC158610	AC158610 Mus muscu
c	82	29.6	20.1	204128	5	AC150904	AC150904 Pan trogl
c	83	29.6	20.1	214578	6	AC164579	AC164579 Mus muscu
c	84	29.6	20.1	227214	15	BX572608	BX572608 Rhodopseu
c	85	29.6	20.1	250218	6	AC158662	AC158662 Mus muscu
	86	29.6	20.1	277754	12	AC055704	AC055704 Mus muscu
	87	29.6	20.1	324050	15	BX251410	BX251410 Tropherym
	88	29.4	20.0	1247	2	AR496391	AR496391 Sequence
	89	29.4	20.0	1247	2	AR511673	AR511673 Sequence
c	90	29.4	20.0	1335	11	BX935907	BX935907 Gallus ga
	91	29.4	20.0	2478	2	CQ589338	CQ589338 Sequence
	92	29.4	20.0	2640	13	AF238306	AF238306 Drosophil
	93	29.4	20.0	2677	13	AY119616	AY119616 Drosophil
c	94	29.4	20.0	3037	11	BC068920	BC068920 Xenopus l
	95	29.4	20.0	5264	2	CQ589337	CQ589337 Sequence
c	96	29.4	20.0	72932	12	AC015300	AC015300 Drosophil
c	97	29.4	20.0	132415	12	AC034276	AC034276 Homo sapi
	98	29.4	20.0	153559	12	AC025000	AC025000 Homo sapi
c	99	29.4	20.0	153559	12	AC025000	AC025000 Homo sapi
	100	29.4	20.0	172281	5	AC068492	AC068492 Homo sapi
	101	29.4	20.0	176735	13	AC007810	AC007810 Drosophil
	102	29.4	20.0	178100	13	AC009742	AC009742 Drosophil
	103	29.4	20.0	212941	13	AE003719	AE003719 Drosophil
	104	29.4	20.0	267739	12	AC169595	AC169595 Bos tauru
	105	29.4	20.0	349142	15	BX572599	BX572599 Rhodopseu
	106	29.2	19.9	4206	15	MAU74385	U74385 Methylomicr
c	107	29.2	19.9	53291	12	AC104745	AC104745 Mus muscu
	108	29.2	19.9	73267	13	CP000171	CP000171 Drosophil
c	109	29.2	19.9	93240	12	AC007586	AC007586 Drosophil
	110	29.2	19.9	99277	12	AC010568	AC010568 Drosophil
	111	29.2	19.9	103842	6	AL840633	AL840633 Mouse DNA
	112	29.2	19.9	104091	13	CP000164	CP000164 Drosophil
	113	29.2	19.9	104875	12	CT009605	CT009605 Danio rer
	114	29.2	19.9	110000	13	AE002665_1	Continuation (2 of
	115	29.2	19.9	110000	13	CP000225_5	Continuation (6 of
c	116	29.2	19.9	110000	13	CP000225_6	Continuation (7 of
	117	29.2	19.9	113098	12	AC009458	AC009458 Drosophil

SCORE Search Results Details for Application :
Search Result us-10-630-536-8.rn

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
start

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                       GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  1, 2006, 03:53:57 ; Search time 886.22 Seconds
                                         (without alignments)
                                         1156.508 Million cell updates/sec

Title:          US-10-630-536-8
Perfect score:  147
Sequence:       1 atttgtcggaaggtcgcagt..........ccgtcagaaagtcatcgacg 147

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :      N_Geneseq_8:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	147	100.0	147	14	ADV04873	Adv04873 Yersinia
c	2	147	100.0	100990	12	ADJ94407	Adj94407 Yersinia
	3	33	22.4	33	14	ADV04872	Adv04872 Yersinia
c	4	31.6	21.5	1641	2	AAQ03677	Aaq03677 Transposa
	5	31.6	21.5	3318	2	AAQ68194	Aaq68194 Tn5099-10
	6	30	20.4	1119	8	ADA69458	Ada69458 Rice gene
	7	30	20.4	1119	12	ADJ39162	Adj39162 Plant cDN
c	8	29.8	20.3	1824	8	ACA35875	Aca35875 Prokaryot
c	9	29.8	20.3	1860	11	ACH95109	Ach95109 Klebsiell
c	10	29.6	20.1	1038	13	ADT49322	Adt49322 Pectate l
c	11	29.6	20.1	1062	14	ACL70895	Acl70895 M. xanthu
	12	29.6	20.1	5467	14	ACL64240	Acl64240 M. xanthu
	13	29.4	20.0	2478	4	ABL13237	Abl13237 Drosophil
	14	29.4	20.0	5264	4	ABL13236	Abl13236 Drosophil
c	15	29	19.7	2413	10	ADE62765	Ade62765 Human gen
	16	28.8	19.6	1275	13	ADO83407	Ado83407 Plant ful
	17	28.8	19.6	1547	12	ADI43237	Adi43237 Plant tra
	18	28.8	19.6	1547	12	ADO62811	Ado62811 Transcrip
c	19	28.6	19.5	126413	11	ACN45068	Acn45068 Mouse gen
	20	28.4	19.3	469	9	ACC73043	Acc73043 Cat flea
	21	28.4	19.3	469	12	ADL09686	Adl09686 Cat flea
	22	28.2	19.2	385	12	ADO03271	Ado03271 Rice orth
	23	28.2	19.2	1278	13	ADT44538	Adt44538 Bacterial
	24	28.2	19.2	1740	14	ACL65980	Acl65980 M. xanthu
	25	28.2	19.2	11620	14	ACL64547	Acl64547 M. xanthu
c	26	28	19.0	4716	14	ACL67316	Acl67316 M. xanthu
	27	28	19.0	23233	14	ACL64721	Acl64721 M. xanthu
c	28	28	19.0	240000	14	ADZ12006	Adz12006 Mouse ste
c	29	27.8	18.9	735	14	ADX55855	Adx55855 Fine chem
c	30	27.8	18.9	1098	13	ADT45872	Adt45872 Bacterial
	31	27.8	18.9	1578	4	AAS54007	Aas54007 Klebsiell
	32	27.8	18.9	4558	2	AAQ43661	Aaq43661 Acetobact
	33	27.6	18.8	909	11	ABD17353	Abd17353 Pseudomon
c	34	27.6	18.8	1221	11	ABD17720	Abd17720 Pseudomon
c	35	27.4	18.6	296	3	AAF09902	Aaf09902 Fusarium
c	36	27.4	18.6	296	13	ADU53943	Adu53943 Fusarium
c	37	27.4	18.6	296	14	ADZ91946	Adz91946 Fusarium
	38	27.4	18.6	324	14	AEB03328	Aeb03328 Mycobacte
	39	27.4	18.6	324	14	AEA79231	Aea79231 Novel M.
c	40	27.4	18.6	906	8	ACA40499	Aca40499 Prokaryot
c	41	27.4	18.6	110000	4	AAI99682_15	Continuation (16 o
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c	43	27.2	18.5	1188	14	ACL68807	Acl68807 M. xanthu
	44	27.2	18.5	2458	2	AAV84801	Aav84801 Nucleotid
	45	27.2	18.5	2458	10	ABT41749	Abt41749 Toxicity
	46	27.2	18.5	2458	13	ADV41663	Adv41663 Rat cardi
c	47	27.2	18.5	30783	14	ACL64795	Acl64795 M. xanthu
	48	27.2	18.5	101241	11	ACN44740	Acn44740 Mouse gen
c	49	27.2	18.5	110000	2	AAV30458_0	Aav30458 Rhizobium
c	50	27.2	18.5	110000	2	AAV30459_0	Aav30459 Rhizobium
c	51	27.2	18.5	110000	4	AAI99682_31	Continuation (32 o
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	54	27	18.4	437	12	ADP57740	Adp57740 Soybean c
	55	27	18.4	1601	13	ADX27274	Adx27274 Plant ful
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	57	27	18.4	10206	8	AAD55182	Aad55182 Megathura
	58	27	18.4	10263	8	AAD55184	Aad55184 Megathura
	59	27	18.4	10495	8	AAD55185	Aad55185 Megathura
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c	63	26.8	18.2	817	2	AAT86824	Aat86824 Hevea bra
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c	65	26.8	18.2	1489	3	AAC77526	Aac77526 Human ORF
	66	26.8	18.2	1657	10	ADD48231	Add48231 Rat gene
	67	26.8	18.2	3342	4	AAH23102	Aah23102 Osteoarth
	68	26.8	18.2	4964	4	AAH18645	Aah18645 Human cDN
c	69	26.6	18.1	507	3	AAA53561	Aaa53561 Human goo
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c	72	26.6	18.1	507	12	ADN59110	Adn59110 Human goo
c	73	26.6	18.1	523	12	ADO21137	Ado21137 Human car
	74	26.6	18.1	546	3	AAA53562	Aaa53562 Human goo
	75	26.6	18.1	546	4	AAH26476	Aah26476 Adrenal g
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	77	26.6	18.1	546	12	ADN59111	Adn59111 Human goo
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c	117	26.6	18.1	3030	4	AAH42268	Aah42268 Nucleotid

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-8.rni.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-8.rni.

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:28:37 ; Search time 180.409 Seconds
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Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a
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    and is derived by analysis of the total score distribution.
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SUMMARIES

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	4	29.6	20.1	5467	3	US-09-902-540-703	Sequence 703, App
	5	29.4	20.0	1247	3	US-09-270-767-1351	Sequence 1351, Ap
	6	29.4	20.0	1247	3	US-09-270-767-16633	Sequence 16633, A
	7	28.8	19.6	601	3	US-09-949-016-80937	Sequence 80937, A
	8	28.8	19.6	601	3	US-09-949-016-80938	Sequence 80938, A
c	9	28.8	19.6	199471	3	US-09-949-016-14083	Sequence 14083, A
	10	28.2	19.2	1740	3	US-09-902-540-2443	Sequence 2443, Ap
	11	28.2	19.2	11620	3	US-09-902-540-1010	Sequence 1010, Ap
c	12	28	19.0	4716	3	US-09-902-540-3779	Sequence 3779, Ap
	13	28	19.0	23233	3	US-09-902-540-1184	Sequence 1184, Ap
	14	27.8	18.9	4558	2	US-08-309-512-2	Sequence 2, Appli
	15	27.8	18.9	4558	7	PCT-US92-08756A-2	Sequence 2, Appli
	16	27.6	18.8	909	3	US-09-252-991A-15957	Sequence 15957, A
c	17	27.6	18.8	1221	3	US-09-252-991A-16324	Sequence 16324, A
c	18	27.4	18.6	296	3	US-09-533-559-2425	Sequence 2425, Ap
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	91	25.4	17.3	203475	3	US-09-949-016-14519	Sequence 14519, A
	92	25.4	17.3	203475	3	US-09-949-016-17226	Sequence 17226, A
	93	25.4	17.3	203475	3	US-09-949-016-17227	Sequence 17227, A
	94	25.4	17.3	203475	3	US-09-949-016-17228	Sequence 17228, A
	95	25.4	17.3	203475	3	US-09-949-016-17229	Sequence 17229, A
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	109	25	17.0	2988	3	US-09-252-991A-5726	Sequence 5726, Ap
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	112	25	17.0	155266	3	US-09-949-016-13870	Sequence 13870, A
c	113	24.8	16.9	307	3	US-09-513-999C-16394	Sequence 16394, A
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c	118	24.8	16.9	3707	3	US-09-902-540-549	Sequence 549, App

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:38:10 ; Search time 2046.39 Seconds
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                 Listing first 150 summaries

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        Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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	5	30	20.4	1119	8	US-10-260-238-162	Sequence 162, App
	6	30	20.4	1119	8	US-10-437-963-92405	Sequence 92405, A
c	7	29.8	20.3	1824	8	US-10-282-122A-23745	Sequence 23745, A
	8	29.4	20.0	2478	13	US-11-097-143-17096	Sequence 17096, A
	9	29.4	20.0	5264	13	US-11-097-143-17095	Sequence 17095, A
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	11	28.8	19.6	606	4	US-09-925-065A-790070	Sequence 790070,
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c	13	28.8	19.6	714	6	US-10-027-632-101701	Sequence 101701,
c	14	28.8	19.6	714	7	US-10-027-632-101701	Sequence 101701,
	15	28.8	19.6	1275	8	US-10-425-114-2127	Sequence 2127, Ap
	16	28.8	19.6	1547	8	US-10-374-780A-1700	Sequence 1700, Ap
	17	28.8	19.6	1862	9	US-10-425-115-19044	Sequence 19044, A
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c	19	28.8	19.6	2274	4	US-09-925-065A-90103	Sequence 90103, A
c	20	28.8	19.6	2274	5	US-09-925-065A-90102	Sequence 90102, A
c	21	28.8	19.6	2274	5	US-09-925-065A-90103	Sequence 90103, A
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c	23	28.8	19.6	2274	12	US-10-301-480-191344	Sequence 191344,
c	24	28.8	19.6	2274	12	US-10-301-480-804752	Sequence 804752,
c	25	28.8	19.6	2274	12	US-10-301-480-804753	Sequence 804753,
c	26	28.8	19.6	2940917	6	US-10-027-632-174763	Sequence 174763,
c	27	28.8	19.6	2940917	7	US-10-027-632-174763	Sequence 174763,
c	28	28.6	19.5	126413	6	US-10-087-192-1831	Sequence 1831, Ap
	29	28.4	19.3	469	8	US-10-621-901-118	Sequence 118, App
	30	28.2	19.2	385	8	US-10-412-699B-1684	Sequence 1684, Ap
	31	28.2	19.2	1278	7	US-10-369-493-42976	Sequence 42976, A
	32	28	19.0	1518	7	US-10-156-761-5098	Sequence 5098, Ap
c	33	28	19.0	150298	10	US-10-981-277-52	Sequence 52, Appl
c	34	28	19.0	164910	10	US-10-981-277-53	Sequence 53, Appl
c	35	28	19.0	196151	10	US-10-981-277-51	Sequence 51, Appl
c	36	28	19.0	240001	10	US-10-936-273-32	Sequence 32, Appl
	37	28	19.0	9025608	7	US-10-156-761-1	Sequence 1, Appli
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	58	27.2	18.5	477	5	US-09-925-065A-541808	Sequence 541808,
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c	60	27.2	18.5	597	8	US-10-767-701-7707	Sequence 7707, Ap
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	63	27.2	18.5	101241	6	US-10-087-192-1339	Sequence 1339, Ap
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	65	27	18.4	437	3	US-09-987-899-809	Sequence 809, App
	66	27	18.4	1601	8	US-10-425-114-10094	Sequence 10094, A
	67	27	18.4	1897	8	US-10-424-599-89297	Sequence 89297, A
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	71	27	18.4	10263	9	US-10-488-824-7	Sequence 7, Appli
c	72	27	18.4	10263	9	US-10-488-824-8	Sequence 8, Appli
	73	27	18.4	10495	9	US-10-488-824-10	Sequence 10, Appl
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	77	26.8	18.2	626	4	US-09-925-065A-885183	Sequence 885183,
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c	99	26.6	18.1	1049	6	US-10-036-342-75	Sequence 75, Appl
c	100	26.6	18.1	1049	6	US-10-036-041-75	Sequence 75, Appl
c	101	26.6	18.1	1049	6	US-10-035-855-75	Sequence 75, Appl
c	102	26.6	18.1	1049	6	US-10-036-214-75	Sequence 75, Appl
c	103	26.6	18.1	1049	6	US-10-035-719-75	Sequence 75, Appl
c	104	26.6	18.1	1049	6	US-10-036-160-75	Sequence 75, Appl
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c	112	26.6	18.1	1049	6	US-10-223-087-319	Sequence 319, App
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c	115	26.6	18.1	1049	7	US-10-035-977-75	Sequence 75, Appl

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-8.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:39:12 ; Search time 152.627 Seconds
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Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
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      and is derived by analysis of the total score distribution.


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                         %
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	6	26.8	18.2	4964	7	US-11-266-748A-58994	Sequence 58994, A
	7	26.8	18.2	97630	7	US-11-266-748A-29025	Sequence 29025, A
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c	10	26.6	18.1	1000	7	US-11-266-748A-405342	Sequence 405342,
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c	12	26.6	18.1	1015	7	US-11-266-748A-31476	Sequence 31476, A
c	13	26.6	18.1	1640	6	US-10-449-902-14082	Sequence 14082, A
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c	15	26	17.7	1242	7	US-11-266-748A-99285	Sequence 99285, A
	16	26	17.7	1242	7	US-11-266-748A-152096	Sequence 152096,
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	45	25	17.0	2558	6	US-10-449-902-22605	Sequence 22605, A
	46	25	17.0	3315	6	US-10-449-902-25062	Sequence 25062, A
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	63	24.6	16.7	473	7	US-11-266-748A-143262	Sequence 143262,
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	75	24.6	16.7	1337	7	US-11-266-748A-316192	Sequence 316192,
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c	81	24.6	16.7	2010	7	US-11-266-748A-354590	Sequence 354590,
c	82	24.6	16.7	2010	7	US-11-266-748A-384942	Sequence 384942,
	83	24.6	16.7	2010	7	US-11-266-748A-437969	Sequence 437969,
c	84	24.6	16.7	2156	7	US-11-266-748A-187932	Sequence 187932,
c	85	24.6	16.7	3350	7	US-11-266-748A-58152	Sequence 58152, A
c	86	24.6	16.7	4253	7	US-11-266-748A-57328	Sequence 57328, A
c	87	24.6	16.7	5726	7	US-11-266-748A-59367	Sequence 59367, A
	88	24.6	16.7	59339	7	US-11-266-748A-23499	Sequence 23499, A
c	89	24.6	16.7	163319	7	US-11-266-748A-23968	Sequence 23968, A
c	90	24.4	16.6	317	7	US-11-266-748A-377210	Sequence 377210,
	91	24.4	16.6	317	7	US-11-266-748A-460589	Sequence 460589,
c	92	24.4	16.6	343	7	US-11-266-748A-306061	Sequence 306061,
c	93	24.4	16.6	422	7	US-11-266-748A-425895	Sequence 425895,
	94	24.4	16.6	499	6	US-10-488-619-2955	Sequence 2955, Ap
	95	24.4	16.6	983	6	US-10-449-902-3932	Sequence 3932, Ap
c	96	24.4	16.6	1366	6	US-10-953-349-27435	Sequence 27435, A
	97	24.4	16.6	1422	6	US-10-449-902-18774	Sequence 18774, A
c	98	24.2	16.5	394	7	US-11-266-748A-302848	Sequence 302848,
c	99	24.2	16.5	827	6	US-10-449-902-8980	Sequence 8980, Ap
	100	24.2	16.5	839	7	US-11-266-748A-371962	Sequence 371962,
	101	24.2	16.5	839	7	US-11-266-748A-389402	Sequence 389402,
c	102	24.2	16.5	839	7	US-11-266-748A-455341	Sequence 455341,
	103	24.2	16.5	955	7	US-11-266-748A-171537	Sequence 171537,
c	104	24.2	16.5	955	7	US-11-266-748A-245364	Sequence 245364,
c	105	24.2	16.5	1721	6	US-10-953-349-1855	Sequence 1855, Ap
	106	24.2	16.5	2030	6	US-10-449-902-4908	Sequence 4908, Ap
	107	24.2	16.5	2257	6	US-10-449-902-26977	Sequence 26977, A
	108	24.2	16.5	2336	6	US-10-449-902-20064	Sequence 20064, A
c	109	24	16.3	729	7	US-11-266-748A-361605	Sequence 361605,
c	110	24	16.3	729	7	US-11-266-748A-387695	Sequence 387695,
	111	24	16.3	729	7	US-11-266-748A-444984	Sequence 444984,
c	112	24	16.3	736	7	US-11-216-545-8129	Sequence 8129, Ap
c	113	24	16.3	811	7	US-11-266-748A-80604	Sequence 80604, A
c	114	24	16.3	811	7	US-11-266-748A-110877	Sequence 110877,
	115	24	16.3	811	7	US-11-266-748A-133415	Sequence 133415,
c	116	24	16.3	1338	7	US-11-217-529-2223	Sequence 2223, Ap
c	117	24	16.3	1820	6	US-10-449-902-25726	Sequence 25726, A
c	118	24	16.3	2602	6	US-10-449-902-28180	Sequence 28180, A
	119	24	16.3	4339	6	US-10-449-902-24429	Sequence 24429, A
	120	23.8	16.2	193	7	US-11-266-748A-427336	Sequence 427336,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-8.rst.

This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-8.rst.

start

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                        GenCore version 5.1.9
             Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          July  1, 2006, 04:17:07 ; Search time 5332.44 Seconds
                                           (without alignments)
                                           1541.534 Million cell updates/sec

Title:           US-10-630-536-8
Perfect score:   147
Sequence:        1 atttgtcggaaggtcgcagt..........ccgtcagaaagtcatcgacg 147

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :       EST:*
                 1:   gb_est1:*
                 2:   gb_est3:*
                 3:   gb_est4:*
                 4:   gb_est5:*
                 5:   gb_est6:*
                 6:   gb_htc:*
                 7:   gb_est2:*
                 8:   gb_est7:*
                 9:   gb_est8:*
                 10:  gb_est9:*
                 11:  gb_gss1:*
                 12:  gb_gss2:*
                 13:  gb_gss3:*
                 14:  gb_gss4:*

         Pred. No. is the number of results predicted by chance to have a
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	32.4	22.0	218	10	N83118	N83118 TgESTzy73g0
	2	32.2	21.9	671	8	CO236707	CO236707 WS0024.B2
c	3	31.4	21.4	614	3	BQ507186	BQ507186 EST614601
c	4	31.4	21.4	614	5	CK861660	CK861660 32764 In
c	5	31	21.1	643	5	CF642183	CF642183 D48_F07 F
c	6	31	21.1	1269	6	CNS0FROA	CR685230 Tetraodon
c	7	30.8	21.0	364	1	AV639843	AV639843 AV639843
	8	30.8	21.0	597	2	BI939652	BI939652 dad27f11.
c	9	30.6	20.8	278	8	CO827214	CO827214 LM_GB5_00
c	10	30.4	20.7	767	14	DU992819	DU992819 OG_ABa011
c	11	30.4	20.7	875	2	BM423055	BM423055 PLATE1_E1
c	12	30.2	20.5	474	5	CD888991	CD888991 G118.1I0L
c	13	30.2	20.5	709	12	CG362920	CG362920 OG2AY29TH
c	14	30.2	20.5	749	2	BJ722261	BJ722261 BJ722261
c	15	30.2	20.5	779	12	CC684152	CC684152 OGOBP18TH
c	16	30.2	20.5	793	12	CG346403	CG346403 OG0GC15TV
	17	30.2	20.5	823	10	DR829764	DR829764 ZM_BFb007
	18	30.2	20.5	836	12	CC335372	CC335372 OGTAH40TV
c	19	30.2	20.5	939	13	CZ384934	CZ384934 ZMMBF0160
c	20	30.2	20.5	941	12	CC383159	CC383159 PUHQC39TB
c	21	30.2	20.5	955	12	CG226597	CG226597 OG0GB14TV
	22	30.2	20.5	956	12	CC383161	CC383161 PUHQC39TD
c	23	30	20.4	1150	10	DW027829	DW027829 CFW241-HO
c	24	29.8	20.3	613	4	CA257585	CA257585 SCCCFL109
c	25	29.8	20.3	809	14	DX024030	DX024030 KBrB018J0
c	26	29.8	20.3	1038	10	DW656520	DW656520 CLJ395-N0
c	27	29.8	20.3	1272	4	CB598012	CB598012 AGENCOURT
c	28	29.6	20.1	420	2	BI727284	BI727284 1031091C0
c	29	29.6	20.1	510	7	BE129451	BE129451 894023C08
c	30	29.6	20.1	517	2	BM000798	BM000798 1031091C0
	31	29.6	20.1	526	8	CN914843	CN914843 030115ABN
	32	29.6	20.1	537	8	CN902820	CN902820 021015ABC
	33	29.6	20.1	577	8	CN914714	CN914714 030110ABN
	34	29.6	20.1	581	8	CN887254	CN887254 010512AAW
c	35	29.6	20.1	654	3	BQ812592	BQ812592 1030031B0
c	36	29.6	20.1	783	10	DT061731	DT061731 AGENCOURT
	37	29.4	20.0	471	8	CO329331	CO329331 EK292624.
c	38	29.4	20.0	516	8	CO344170	CO344170 EP18764.3
	39	29.4	20.0	608	8	CN897524	CN897524 010701AAZ
c	40	29.4	20.0	622	2	BJ071236	BJ071236 BJ071236
c	41	29.4	20.0	690	10	DT055649	DT055649 AGENCOURT
c	42	29.4	20.0	692	8	CN130245	CN130245 RHOH1_40_
c	43	29.4	20.0	695	10	DT062641	DT062641 AGENCOURT
	44	29.4	20.0	851	10	DR560924	DR560924 WS02620.C
c	45	29.4	20.0	857	3	BU901960	BU901960 AGENCOURT
c	46	29.4	20.0	902	4	CA972665	CA972665 AGENCOURT
c	47	29.4	20.0	987	14	CNS079PI	AL435580 T7 end of
	48	29.2	19.9	538	5	CK349793	CK349793 hggfha18A
	49	29.2	19.9	588	4	CB375197	CB375197 ru98g01.y
	50	29.2	19.9	612	11	BZ250355	BZ250355 CH230-448
	51	29.2	19.9	650	9	CX353284	CX353284 ssalrgb53
	52	29.2	19.9	748	14	DX103828	DX103828 MUGQ_CH25
	53	29.2	19.9	770	5	CK351523	CK351523 hggfha39D

c	54	29.2	19.9	779	5	CK187745	CK187745 EST777060
c	55	29.2	19.9	781	12	CG287393	CG287393 OG0BH92TH
c	56	29.2	19.9	817	5	CK699860	CK699860 ZF101-P00
c	57	29.2	19.9	832	12	BZ799294	BZ799294 PUFGN83TD
c	58	29.2	19.9	844	12	CG377903	CG377903 OGYAR73TV
c	59	29.2	19.9	847	12	CG276600	CG276600 OGZBG93TH
	60	29.2	19.9	849	12	CG287400	CG287400 OG0BH92TV
c	61	29	19.7	653	2	BI956991	BI956991 HVSMEn000
c	62	29	19.7	1017	11	BZ563071	BZ563071 pacs2-164
	63	28.8	19.6	323	1	AA084793	AA084793 zn13b01.r
c	64	28.8	19.6	388	2	BJ922159	BJ922159 BJ922159
c	65	28.8	19.6	423	10	N81852	N81852 TgESTzy48h0
	66	28.8	19.6	430	1	AM138865	AM138865 AM138865
	67	28.8	19.6	435	2	BJ909573	BJ909573 BJ909573
	68	28.8	19.6	519	1	AM139451	AM139451 AM139451
	69	28.8	19.6	567	13	CZ793062	CZ793062 OC__Ba016
c	70	28.8	19.6	573	4	CB389408	CB389408 OSTF116G7
	71	28.8	19.6	613	10	DV546594	DV546594 rbcma0_00
	72	28.8	19.6	690	8	CN476307	CN476307 SPVD11d08
c	73	28.8	19.6	691	9	DN096532	DN096532 JGI_CABE6
	74	28.8	19.6	705	9	DR093951	DR093951 STRR1_11_
c	75	28.8	19.6	724	2	BJ538110	BJ538110 BJ538110
c	76	28.8	19.6	736	2	BJ534435	BJ534435 BJ534435
c	77	28.8	19.6	745	2	BJ541750	BJ541750 BJ541750
	78	28.8	19.6	749	3	BW447274	BW447274 BW447274
	79	28.8	19.6	749	9	DR093883	DR093883 STRR1_11_
c	80	28.8	19.6	766	2	BJ723178	BJ723178 BJ723178
c	81	28.8	19.6	792	9	DR020365	DR020365 STRS1_36_
	82	28.8	19.6	798	9	DR100271	DR100271 STRR1_63_
c	83	28.8	19.6	808	9	DR101188	DR101188 STRR1_71_
c	84	28.8	19.6	817	2	BG719203	BG719203 602690258
	85	28.8	19.6	818	9	CX806778	CX806778 JGI_CAAJ1
	86	28.8	19.6	830	9	DR100474	DR100474 STRR1_64_
c	87	28.8	19.6	836	9	DR025068	DR025068 STRS1_69_
	88	28.8	19.6	839	9	CX713116	CX713116 RTPQ1_7_C
	89	28.8	19.6	840	9	CX713197	CX713197 RTPQ1_7_C
	90	28.8	19.6	840	9	DR016857	DR016857 STRS1_12_
	91	28.8	19.6	845	9	DR097239	DR097239 STRR1_33_
c	92	28.8	19.6	858	9	DR020300	DR020300 STRS1_36_
c	93	28.8	19.6	890	9	CX814195	CX814195 JGI_CAAJ2
c	94	28.8	19.6	944	2	BJ741548	BJ741548 BJ741548
	95	28.6	19.5	276	3	BP383858	BP383858 BP383858
c	96	28.6	19.5	379	3	BQ074085	BQ074085 fz31e09.y
	97	28.6	19.5	417	8	CO189699	CO189699 EK044927.
	98	28.6	19.5	545	10	DV228474	DV228474 EST-AR162
	99	28.6	19.5	574	14	DE050917	DE050917 Oryzias 1
c	100	28.6	19.5	578	11	AQ600063	AQ600063 HS_5354_B
c	101	28.6	19.5	582	8	CV439602	CV439602 EST893515
c	102	28.6	19.5	610	9	DA531428	DA531428 DA531428
	103	28.6	19.5	752	10	DR645264	DR645264 EST103588
c	104	28.6	19.5	806	11	BH707579	BH707579 BOMNO31TF
	105	28.6	19.5	895	10	DR675509	DR675509 EST106562
	106	28.6	19.5	901	2	BG251828	BG251828 602364443
	107	28.6	19.5	919	10	DR645378	DR645378 EST103600
	108	28.6	19.5	942	10	DR660636	DR660636 EST105075
c	109	28.6	19.5	1097	9	DR135739	DR135739 49291272
	110	28.6	19.5	1156	10	DW037105	DW037105 CFW270-C0
	111	28.4	19.3	210	8	CX244595	CX244595 A59 cDNA-
c	112	28.4	19.3	346	4	BY021829	BY021829 BY021829
c	113	28.4	19.3	432	4	CB543200	CB543200 PVEPSE302
	114	28.4	19.3	459	3	BP175592	BP175592 BP175592